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(71) Applicant: PRIZM PHARMACEUTICALS, INC. [US/US]; 11035 Roselle Street, San Diego, CA 92121-1204 (US).

(72) Inventors: SOSNOWSKI, Barbara, A.; 1013 Adella Avenue, Coronado, CA 92118 (US). VICTOR, Kimberly, D., 1865 Willow Way, Vista, CA 92083 (US). HOUSTON, L., L.; 4045 Carmel View #92, Del Mar, CA 92014 (US). NOVA, Michael, P.; P.O. Box 3023, Rancho Sante Fe, CA 92067 (US). FREUND, Erwin; 2915 Sunset Hills, Escondido, CA 92025 (US). FLEURBAAII, Graham, A.; 10674 Eglantine Court, San Diego, CA 92131 (US).

(74) Agents: NOTTENBURG, Carol et al.; Seed and Berry, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).

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(54) Title: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGETED AGENTS

#### (57) Abstract

Conjugates of vascular endothelial growth factor (VEGF) linked, either directly or via a linker, to a targeted agent are provided. The targeted agent is a cytotoxic agent, such as a ribosome-inactivating protein (RIP) and an antisense nucleic acid, or is a therapeutic nucleic acid for targeted delivery to vascular endothelial cells. The targeted agent is attached to VEGF, or via a linker, through a chemical bond, or the conjugate is prepared as a chimera using techniques of recombinant DNA. The conjugates are used to target cytotoxic agents or therapeutic nucleotides to endothelial cells and are particularly useful for treating solid tumors, such as Kaposi's sarcoma, and for treating ophthalmic disorders with underlying vascular proliferation.

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#### Description

# CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGETED AGENTS

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#### Technical Field

The present invention relates to the treatment of diseases, and more specifically, to the preparation of conjugates of a vascular endothelial cell growth factor and a targeted agent, and their use in altering the function, gene-expression, or viability of a cell in a therapeutic manner.

#### Background of the Invention

A major goal of treatment of neoplastic diseases and hyperproliferative disorders is to ablate the abnormally growing cells while leaving normal cells untouched. Various methods are under development for providing treatment, but none provide the requisite degree of specificity.

One method of treatment is to deliver toxins to appropriate targets. Immunotoxins and cytotoxins are protein conjugates of toxin molecules with either antibodies or factors which bind to receptors on target cells. Three major problems may limit the usefulness of immunotoxins. First, the antibodies may react with more than one cell surface molecule, thereby effecting delivery to multiple cell types, possibly including normal cells. Second, even if the antibody is specific, the antibody reactive molecule may be present on normal cells. Third, the toxin molecule may be toxic to cells prior to delivery and internalization. Cytotoxins suffer from similar disadvantages of specificity and toxicity. Another limitation in the therapeutic use of immunotoxins and cytotoxins is the relatively low ratio of therapeutic to toxic dosage. Additionally, it may be difficult to direct sufficient concentrations of the toxin into the cytoplasm and intracellular compartments in which the agent can exert its desired activity.

Given these limitations, cytotoxic therapy has been attempted using viral vectors to deliver DNA encoding the toxins into cells. If eukaryotic viruses are used, such as the retroviruses currently in use, they may recombine with host DNA to produce infectious virus. Moreover, because retroviral vectors are often inactivated by the complement system, use *in vivo* is limited. Retroviral vectors also lack specificity in delivery; receptors for most viral vectors are present on a large fraction, if not all, cells. Thus, infection with such a viral vector will infect normal as well as abnormal

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cells. Because of this general infection mechanism, it is not desirable for a viral vector to directly encode a cytotoxic molecule.

While delivery of nucleic acids offers advantages over delivery of cytotoxic proteins such as reduced toxicity prior to internalization, there is a need for high specificity of delivery, which is currently unavailable with the present systems.

In view of the problems associated with gene therapy, there is a compelling need for improved treatments which are more effective and are not associated with such disadvantages. The present invention exploits the use of conjugates which have increased specificity and deliver higher amounts of nucleic acids to targeted cells, while providing other related advantages.

#### Summary of the Invention

The present invention generally provides conjugates of vascular endothelial cell growth factor (VEGF) polypeptide or a portion thereof and a targeted In one embodiment of this invention, the VEGF and targeted agent are conjugated through a linker. Within each conjugate, there can be more than one VEGF and targeted agent molecule. Preferably, in the conjugates, there are between one and six VEGF and targeted agents, and most preferably one VEGF molecule and one targeted agent conjugated prior to dimerization. In certain embodiments, the linker is 20 selected from the group consisting of protease substrates, linkers that increase the flexibility of the conjugate, linkers that increase the solubility of the conjugate, photocleavable linkers and acid cleavable linkers. In certain other embodiments, the VEGF polypeptide may be native human or bovine VEGF or VEGF, which is modified by addition of a cysteine residue or replacement of a nonessential amino acid residue within about 20 amino acids of the N-terminus or C-terminus. In vet other embodiments, the targeted agent is cytotoxic, preferably a ribosome inactivating protein, and most preferably saporin. Other cytotoxic agents include methotrexate. anthrocyclines, Pseudomonas exotoxin, porphyrin, or a nucleic acid.

In another embodiment, the conjugate has the formula: targeted agent- $(L)_q$ -VEGF- $(L)_r$ -VEGF, wherein q and r, which may be the same or different, are 0 or 1. In vet another embodiment, the conjugate has the formula: targeted agent-(L)<sub>Q</sub>-VEGF.

In other aspects, methods of targeting an agent to cells bearing VEGF receptors, comprises conjugating the targeted agent to one or more VEGF monomers or portions thereof that bind to a VEGF receptor, whereby the conjugated targeted agent is internalized by the cells. In another aspect, methods of treating VEGF-mediated pathophysiological conditions, comprising administering to the animal a therapeutically

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effective amount of a conjugate between VEGF and a cytotoxic agent, are provided. In certain embodiments, the condition is a dermatological disorder with underlying vascular proliferation, a solid tumor, or an ophthalmic disorder, such as diabetic retinopathy, proliferative vitreoretinopathy, and pterygium. The dermatological disorder is Kaposi's sarcoma, psoriasis or macular degeneration. Methods are also provided to inhibit proliferation of cells bearing VEGF receptors, comprising contacting the cells with an effective amount of a VEGF targeted agent conjugate.

In yet other aspects, methods of effecting gene therapy are provided, wherein cells are contacted with a conjugate having a targeted agent which is a nucleic acid, and the conjugate includes a nuclear translocation sequence linked to the targeted nucleic acid or VEGF.

In yet other aspects, DNA fragments, encoding a conjugate between a targeted agent and VEGF are provided. In certain embodiments, the DNA conjugate may additionally comprise a linker. Plasmids, vectors, and host cells are also provided. In another embodiment, methods of producing conjugate of VEGF and a targeted agent comprising growing a culture of cells transformed with a vector containing a VEGF cytotoxic agent conjugate whereby DNA is transcribed and translated to produce the conjugate are provided.

In other embodiments, the VEGF monomer that is modified by insertion of a cysteine residue within about 20 amino acids of the N-terminus or C-terminus. wherein the inserted residue replaces a nonessential residue in the unmodified VEGF monomer is provided.

Pharmaceutical compositions, comprising the VEGF targeted agent conjugate and a physiological acceptable excipient are also provided.

These and other aspects of the present invention will become evident upon reference to the following detailed description and attached drawings. In addition, various references are set forth below which describe in more detail certain procedures or compositions, and are therefore incorporated by reference in their entirety.

## 30 Brief Description of the Drawings

Figure 1 is a Coomassie blue stained polyacrylamide-SDS gel and Western blot analyses of VEGF production using the  $pP_L$ - $\lambda$  expression system. Inclusion bodies were isolated from bacteria by the addition of lysozyme followed by centrifugation. Equal amounts of each sample were run under reducing conditions. An antibody to an N-terminus peptide of VEGF (Oncogene Sciences) was used in the Western analysis. Lanes 1 and 5. VEGF<sub>165</sub> t=0 hours post-induction: lanes 3 and 7. VEGF<sub>121</sub> t=0 hours post-induction: lanes 2 and 6. VEGF<sub>165</sub> t=2 hours post-induction:

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lanes 4 and 8, VEGF<sub>121</sub> t=2 hours post-induction. Proteins of expected molecular weights of 19.2 kD for monomeric VEGF<sub>165</sub> and 14.2kD for monomeric VEGF<sub>121</sub> were observed.

Figure 2 is a Coomassie blue stained polyacrylamide-SDS gel analysis of VEGF<sub>121</sub> and VEGF<sub>165</sub> under reducing and non-reducing conditions. Inclusion bodies were isolated and VEGF refolded and dimerized under the given conditions. Lanes 1 and 3, VEGF<sub>121</sub>; lanes 2 and 4, VEGF<sub>165</sub>. The predicted molecular weights for VEGF<sub>121</sub> are 14.2 kD and 28.4 kD for monomeric and dimeric forms respectively. The predicted molecular weights for VEGF<sub>165</sub> are 19.2 kD and 38.4 kD for monomeric and dimeric forms respectively.

Figure 3 is a graph of the results of an acid phosphate assay, which measures viable cell members, showing that purified VEGF<sub>121</sub> or VEGF<sub>165</sub> made in *E. coli* can stimulate proliferation of HMVEC (human microvascular endothelial cells). VEGF<sub>121</sub> and VEGF<sub>165</sub> were isolated from inclusion bodies and tested for their ability to induce proliferation of HMVEC. *E. coli* derived material is shown in comparison to either VEGF<sub>121</sub> or VEGF<sub>165</sub> produced in insect cells (R&D, BV). Both forms of VEGF produced in *E. coli* induce proliferation of HMVEC in a dose dependent manner at concentrations as low as 10-11 to 10-10M. VEGF<sub>121</sub> produced in *E. coli* is more potent than VEGF<sub>121</sub> produced in insect cells, while VEGF<sub>165</sub> made in *E. coli* is less active.

Figure 4 is a Coomassie blue stained polyacrylamide-SDS gel and Western blot analysis of VEGF-SAP mitotoxin production using the  $pP_L$ - $\lambda$  expression system. Inclusion bodies were isolated from bacteria by the addition of lysozyme followed by centrifugation. Equal amounts of each sample were run under reducing conditions. An antibody to an N-terminus peptide of saporin was used in the Western analysis. Lanes 1 and 3, VEGF<sub>121</sub>-SAP; lanes 2 and 4, VEGF<sub>165</sub>-SAP. Proteins of expected molecular weights of 42.2 kD for VEGF<sub>121</sub>-SAP and 47.2 kD for VEGF<sub>165</sub>-SAP were observed.

Figure 5 is a Coomassie blue stained polyacrylamide-SDS gel of VEGF<sub>121</sub>-SAP run under reducing and non-reducing conditions. Inclusion bodies were isolated and VEGF<sub>121</sub>-SAP refolded under the given conditions. The predicted molecular weight for VEGF<sub>121</sub>-SAP is 42.2 kD under reducing conditions.

Figure 6 is a graph depicting inhibition of protein synthesis in a cell-free system. The effect of VEGF<sub>121</sub>-SAP on protein synthesis in a cell-free luciferase system was compared to that of SAP.

Figure 7 is a graph showing that VEGF<sub>165</sub>-SAP inhibits proliferation of HMVEC (human microvascular endothelial cells) in a dose dependent manner. CCSV.

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chemical conjugate VEGF<sub>165</sub>-SAP; FPSV, SAP-VEGF<sub>121</sub> made in *E. coli* from inclusion bodies; VEGF<sub>121</sub>, insect cell derived.

#### Detailed Description of the Invention

#### **Definitions**

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the subject matter herein belongs.

The "amino acids" are identified according to their well-known, three-letter or one-letter abbreviations. The nucleotides, which occur in the various DNA fragments, are designated with the standard single-letter designations used routinely in the art.

As used herein, to "bind to a receptor" refers to the ability of VEGF to detectably bind to such receptors as assayed by standard *in vitro* assays. For example, binding measures the capacity of a VEGF conjugate, VEGF monomer, or VEGF dimer to recognize the VEGF receptor on vascular endothelial cells, such as an aortic vascular endothelial cell line using a procedure such as the one described in Moscatelli (*J. Cell Physiol. 131*:123-130, 1987). Briefly, cells are grown to subconfluence and incubated in appropriate buffer with radioiodinated VEGF dimer in the presence of various concentrations of the VEGF monomer or dimer or VEGF conjugate of interest. Binding affinity is measured by counting the membrane fraction that is solubilized in a suitable buffer containing a detergent, such as in 0.5% Triton X-100 in PBS (pH 8.1).

As used herein, "biological activity" refers to the in vivo activities of a compound or physiological responses that result upon in vivo administration of a compound, composition or other mixture. Biological activity, thus, encompasses therapeutic effects and pharmaceutical activity of such compounds, compositions and Such biological activity may, however, be defined with reference to mixtures. particular in vitro activities, as measured in a defined assay. Thus, for example, reference herein to the biological activity or reactivity of VEGF, a dimer thereof. monomer, or fragment thereof, or other combination of VEGF monomers and fragments, refers to the ability of the VEGF to bind to cells bearing VEGF receptors and internalize a linked agent. Such activity is typically assessed in vitro by linking the VEGF (dimer, monomer or fragment) to a cytotoxic agent, such as saporin, contacting cells bearing VEGF receptors, such as aortic endothelial cells, with the conjugate and assessing cell proliferation or growth. In vivo activity may be assessed using recognized animal models, such as the mouse xenograft model for anti-tumor activity (see. e.g., Beitz et al. (1992) Cancer Research 52:227-230; Houghton et al. (1982)

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Cancer Res. 42:535-539; Bogden et al. (1981) Cancer (Philadelphia) 48:10-20; Hoogenhout et al. (1983) Int. J. Radiat. Oncol., Biol. Phys. 9:871-879; Stastny et al. (1993) Cancer Res. 53:5740-5744).

As used herein, a "conjugate" refers to a molecule that contains at least one VEGF moiety and at least one targeted agent that are linked directly or via a linker and that are produced by chemical coupling methods or by recombinant expression of chimeric DNA molecules to produce fusion proteins.

As used herein, the term "cytotoxic agent" refers to a molecule capable of inhibiting cell function. The agent may inhibit cell growth, differentiation or proliferation or be toxic to cells. The term includes agents whose toxic effects are mediated only when transported into the cell and also those whose toxic effect is mediated at the cell surface. A variety of cytotoxic agents can be used and include those that inhibit protein synthesis and those that inhibit expression of certain genes essential for cell growth or survival.

As used herein, "DNA encoding a VEGF peptide or polypeptide" refers to any of the DNA fragments set forth herein as coding such peptides, to any such DNA fragments known to those of skill in the art, any DNA fragment that encodes a VEGF that binds to a VEGF receptor and is internalized thereby. Such a DNA molecule may be isolated from a human cell library using any DNA fragment that encodes any of the VEGF peptides set forth in SEQ ID NOs. 25-28 or any DNA fragment that may be produced from any of the preceding DNA fragments by substitution of degenerate codons. It is understood that once the complete amino acid sequence of a peptide, such as a VEGF peptide, is available to those of skill in this art, it is routine to substitute degenerate codons and produce any of the possible DNA fragments that encode such peptide. It is also generally possible to synthesize DNA encoding such peptide based on the amino acid sequence.

As used herein, a "fusion protein" refers to a polypeptide that contains at least two components, such as VEGF and a targeted agent or VEGF and linker, and is produced by expression of DNA in a host cell.

As used herein, "nucleic acids" refer to RNA or DNA that are intended as targeted agents, which include, but are not limited to. DNA encoding therapeutic proteins, fragments of DNA for co-suppression, DNA encoding cytotoxic proteins, antisense nucleic acids and other such molecules. Reference to nucleic acids includes duplex DNA, single-stranded DNA, RNA in any form, including triplex, duplex or single-stranded RNA, anti-sense RNA, polynucleotides, oligonucleotides, single nucleotides and derivatives thereof.

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Nucleic acids may be composed of the well-known deoxyribonucleotides or ribonucleotides composed of the bases: adenosine, cytosine, guanine, thymidine, and uridine. As well, various other nucleotide derivatives and non-phosphate backbones or phosphate derivative backbones may be used.

For example, because normal phosphodiester oligonucleotides (referred to as PO oligonucleotides or type I; see structure, below, where X = 0) are sensitive to DNA- and RNA-specific nucleases, several resistant types of oligonucleotides have been developed (see, e.g., International Application WO 93/23570, which is based on 07/881,255, filed May 11, 1992; International Application WO 93/15742, which is based on 07/833,146, filed February 10, 1992; Wagner et al. (1993) Science 260:1510-1514; U.S. Patent No. 5,218,088, U.S. Patent No. 5,175,269; U.S. Patent No. 5,109,124; Carter et al. (1993) Br. J. Cancer 67:869-876); these include types II-IV:

in which B is a nucleotide base; and X is OEt in phosphotriester (type II), X is Me in methylphosphonate (type III; referred to as MP oligos); and X is S in phosphorothicate (referred to as PS oligos; U.S. Patent No. 5,218,088 to Gorenstein et al. describes a method for preparation of PS oligos). Presently, MP and PS oligonucleotides have been the focus of most investigation.

As used herein, the term "VEGF" refers to any polypeptide that, either as a monomer or dimer, binds to a VEGF receptor and is transported into the cell by virtue of

its interaction with the receptor. A polypeptide that is "reactive" with the receptor binds to the receptor and is internalized. VEGF refers to peptides having amino acid sequences of native VEGF polypeptide monomers, as well as VEGF polypeptides modified by amino acid substitutions, deletions, insertions or additions in the native protein, but alone or linked to a targeted agent retains the ability to bind to a VEGF receptor and to be internalized in a cell bearing such receptor. Such polypeptides include, but are not limited to human VEGF121, human VEGF165, human VEGF189. human VEGF189, bovine VEGF189, bovine VEGF189, and homodimers and heterodimers of any VEGF monomer or monomers. In addition, peptides reactive with VEGF receptors that are isolated by phage display (U.S. Patent No. 5,223,409 and 5,403,484) are encompassed as well. It is understood that differences in amino acid sequences can occur among VEGFs of different species as well as among VEGFs from individual organisms or species and that such minor allelic variations or variations among species are intended to be encompassed by

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reference to VEGF herein. As used herein a "portion of a VEGF" refers to a fragment or piece of VEGF that is sufficient, either alone or as a dimer with another fragment or a VEGF polypeptide, to bind to a VEGF receptor and internalize a linked targeted agent.

Muteins of VEGF include, but are not limited to, those produced by replacing one or more of the cysteines with serine as herein or those that have any other amino acids deleted or replaced. Typically, muteins will have conservative amino acid changes, such as those set forth below in Table 1. DNA encoding such muteins will, unless modified by replacement of degenerate codons, hybridize under conditions of at least low stringency to DNA encoding a VEGF (SEQ ID NOs. 25-28) or an exon thereof (SEQ ID NOs. 16-24). VEGF may be isolated from natural sources or be made synthetically, such as by recombinant means or chemical synthesis.

As used herein, "VEGF-mediated pathophysiological condition" refers to a deleterious condition characterized by or caused by proliferation of cells that are sensitive to VEGF mitogenic stimulation.

As used herein, "VEGF receptors" refer to receptors that react with a naturally-occurring member of the VEGF family of proteins and transport it into a cell bearing such receptors. Included among these are the fms-like tyrosine kinase receptor (FLT) and the kinase insert domain-containing receptor (KDR) (see. e.g., International Application WO 92/14748, which is based on U.S. Applications Serial No. 08/657,236, de Vries et al. (1992) Science 255:989-91; Terman et al. (1992) Biochem. Biophys. Res. Commun. 187:1579-1586; Kendall et al. (1993) Proc. Natl. Acad. Sci. USA 90:10705-10709; and Peters et al. (1993) Proc. Natl. Acad. Sci. USA 90:8915-8919).

As used herein, a "targeted agent" is any agent that is intended for internalization by linkage to VEGF, and that upon internalization alters or affects cellular metabolism, growth, activity, viability or other property or characteristic of the cell. The targeted agents include proteins, polypeptides. organic molecules, drugs, nucleic acids and other such molecules. As used herein, to target a targeted agent, such as a cytotoxic agent, means to direct it to a cell that expresses a selected receptor by linking the agent to a polypeptide reactive with a VEGF receptor.

As used herein, a "therapeutic nucleic acid" describes any nucleic acid used in the contest of invention that modify gene transcription or translation. This term also includes nucleic acids that bind to sites on proteins and to receptors. It includes, but is not limited to the following types of nucleic acids: nucleic acids encoding a protein, antisense RNA, DNA intended to form triplex molecules, extracellular protein binding oligonucleotides and small nucleotide molecules. A therapeutic nucleic acid may serve as a replacement for a defective gene or encode a therapeutic product, such

as TNF or a cytoxic molecule, such as saporin. The therapeutic nucleic acid may encode all or a portion of a gene, and may function by recombining with DNA already present in a cell, thereby replacing a defective portion of a gene. It may also encode a portion of a protein and exert its effect by virtue of co-suppression of a gene product.

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#### A. Vascular endothelial growth factors

### 1. Polypeptides reactive with a VEGF receptor

Vascular endothelial growth factors (VEGFs) were identified by their ability to directly stimulate endothelial cell growth, but do not appear to have mitogenic effects on other types of cells. VEGFs also cause a rapid and reversible increase in blood vessel permeability. The members of this family have been referred to variously as vascular endothelial growth factor (VEGF), vascular permeability factor (VPF) and vasculotropin (see, e.g., Plouet et al., EMBO J. 8:3801-3806, 1989). Herein, they are collectively referred to as VEGF.

VEGF was originally isolated from a guinea pig heptocarcinoma cell line, line 10, (see, e.g., U.S. Patent No. 4,456,550) and has subsequently been identified in humans and in normal cells. It is expressed during normal development and in certain normal adult organs. Purified VEGF is a basic, heparin-binding, homodimeric glycoprotein that is heat-stable, acid-stable and may be inactivated by reducing agents.

DNA sequences encoding VEGF and methods to isolate these sequences may be found primarily in U.S. Patent No. 5,240,848, U.S. Patent No. 5,332,671, U.S. Patent No. 5,219,739, U.S. Patent No. 5,194,596, and Houch et al., *Mol. Endocrin.* 5:180, 1991.

VEGF family members arise from a single gene organized as eight 25 exons and spanning approximately 14 kb in the human genome. Four molecular species of VEGF result from alternative splicing of mRNA and contain 121, 165, 189 and 206 amino acids. The four species have similar biological activities, but differ markedly in their secretion patterns. The predominant isoform secreted by a variety of normal and transformed cells is VEGF165. Transcripts encoding VEGF121 and VEGF<sub>189</sub> are detectable in most cells and tissues that express the VEGF gene. In 30 contrast, VEGF206 is less abundant and has been identified only in a human fetal liver cDNA library. VEGF<sub>121</sub> is a weakly acidic polypeptide that lacks the heparin binding domain and, consequently, does not bind to heparin. VEGF189 and VEGF206 are more basic than VEGF<sub>165</sub> and bind to heparin with greater affinity. Although not every identified VEGF isoform binds heparin, all isoforms are considered to be 35 heparin-binding growth factors within the context of this invention.

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The secreted isoforms, VEGF<sub>121</sub> and VEGF<sub>165</sub> are preferred VEGF proteins. VEGF<sub>121</sub> is particularly preferred. The longer isoforms, VEGF<sub>189</sub> and VEGF<sub>206</sub>, are almost completely bound to the extracellular matrix and need to be released by an agent, such as urokinase, suramin, heparin or heparinase, and plasmin. Other preferred VEGF proteins contain various combinations of VEGF exons, such that the protein still binds VEGF receptor and is internalized. It is not necessary that a VEGF protein used in the context of this invention either retain any of its *in vivo* biological activities, such as stimulating endothelial cell growth, or bind heparin. It is only necessary that the VEGF protein or fragment thereof bind the VEGF receptor and be internalized into the cell bearing the receptor. However, it may be desirable in certain contexts for VEGF to manifest certain of its biological activities. For example, if VEGF is used as a carrier for DNA encoding a molecule useful in wound healing, it would be desirable that VEGF exhibit vessel permeability activity and promotion of fibroblast migration and angiogenesis. It will be apparent from the teachings provided within the subject application which of the activities of VEGF are desirable to maintain.

VEGF promotes an array of responses in endothelium, including blood vessel hyperpermeability, endothelial cell growth, angiogenesis, cell migration and enhanced glucose transport. VEGF stimulates the growth of endothelial cells from a variety of sources (including brain capillaries, fetal and adult aortas, and umbilical veins) at low concentrations, but is reported to have no effect on the growth of vascular smooth muscle cells, adrenal cortex cells, keratinocytes, lens epithelial cells, or BHK-21 fibroblasts. VEGF also is a potent polypeptide regulator of blood vessel function; it causes a rapid but transient increase in microvascular permeability without causing endothelial cell damage or mast cell degranulation, and its action is not blocked by antihistamines. VEGF has also been reported to induce monocyte migration and activation and has been implicated as a tumor angiogenesis factor in some human gliomas. Also, VEGF is a chemoattractant for monocytes and VEGF has been shown to enhance the activity of the inflammatory mediator tumor necrosis factor (TNF).

Quiescent and proliferating endothelial cells display high-affinity binding to VEGF, and endothelial cell responses to VEGF appear to be mediated by high affinity cell surface receptors. Two tyrosine kinases have been identified as VEGF receptors. The first, known as fms-like tyrosine kinase or FLT is a receptor tyrosine kinase that is specific for VEGF. In adult and embryonic tissues, expression of FLT mRNA is localized to the endothelium and to populations of cells that give rise to endothelium. The second receptor KDR (human kinase insert domain-containing receptor), and its mouse homologue FLK-1, are closely related to FLT. The KDR/FLK-1 receptor is expressed in endothelium during the fetal growth stage, during

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earlier embryonic development, and in adult tissues. In addition, messenger RNA encoding FLT and KDR have been identified in tumor blood vessels and specifically by endothelial cells of blood vessels supplying glioblastomas. Similarly, FLT and KDR mRNAs are upregulated in tumor blood vessels in invasive human colon adenocarcinoma, but not in the blood vessels of adjacent normal tissues.

VEGF suitable for use herein also includes any polypeptide or fragment of a VEGF protein that retains the ability, either as a monomer or as part of a dimer, to bind to a VEGF receptor and to be internalized by a cell bearing such receptor. In addition, VEGF include any combination of peptides encoded by the exons set forth in SEQ ID NOs. 16-24 that retains the requisite receptor binding and internalization activities. Amino acid sequence variations in VEGF, including allelic variations and conservative amino acid substitutions, such as those set forth in TABLE 1, that do not alter its ability to bind to VEGF receptors and to be internalized by cells upon such binding are suitable for use in the present invention.

The various VEGF isoforms that result from alternative splicing of RNA transcribed from a VEGF gene (see, e.g., U.S. Patent No. 5,219,739 to Tischer et al.; U.S. Patent No. 5,194,596 to Tisher et al.; U.S. Patent No. 5,240,848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications nos. 07/351,361, 07/369,424, 07/389,722, to Genentech, Inc., and U.S. applications Serial Nos. 07/351,361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 A1 and EP 0 476 983 A1 to Merck & Co.; Houck et al. (1991) Mol. Endo. 5:1806-1814; see also SEQ ID Nos. 18-28; see, also SEQ ID Nos. 86-89, for modified forms produced herein) are also suitable for use in the present invention.

Any polypeptide that is reactive with a VEGF receptor may be used in the present invention. VEGF conjugates preferably include at least two VEGF monomers in an antiparallel orientation. Dimer formation occurs when VEGF monomers are mixed under physiological or other appropriate conditions. Also, expression of tandem repeats of VEGF as fusion proteins, with or without linkers separating the monomers, should result in dimers upon expression of DNA encoding the VEGF fusion proteins.

VEGF may be isolated from any mammalian source, including human, bovine and murine sources, although human is preferred. The VEGF polypeptides include those that, when dimerized, are mitogenic to vascular endothelial cells. Mitogenic activity, however, is not required for the VEGF moieties used herein. It is sufficient that the polypeptide, bind to a VEGF receptor and internalize a linked agent.

#### 2. Modifications of VEGF

The preferred VEGF molecules are those that are set forth in SEQ ID Nos. 25-28 or peptides that have minor sequence variations of the peptides. Such minor sequence variations include, but are not limited to, minor allelic or species variations and insertions or deletions of residues, particularly cysteine residues. Suitable conservative substitutions of amino acids are known to those of skill in this art and may be made generally without altering the biological activity of the resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity (see, e.g., Watson et al. Molecular Biology of the Gene, 4th Edition, 1987, The Benjamin/Cummings Pub. Co., p.224). Such substitutions are preferably made in accordance with those set forth in TABLE 1 as follows:

TARLE 1

Original Residue	Conservative substitution
Ala (A)	Gly; Ser
Arg (R)	Lys
Asn (N)	Gln; His
Cys (C)	Ser; neutral amino acid
Gln (Q)	Asn
Glu (E)	Asp
Gly (G)	Ala; Pro
His (H)	Asn: Gin
Ile (I)	Leu; Val
Leu (L)	Ile; Val
Lys (K)	Arg; Gln; Glu
Met (M)	Leu; Tyr; Ile
Phe (F)	Met; Leu: Tyr
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr
Tyr (Y)	Trp: Phe
Val (V)	Ile; Leu

Other substitutions are also permissible and may be determined empirically or in accord with known conservative substitutions. Any such modification of the polypeptide may be effected by any means known to those of skill in this art.

VEGF peptides include those having SEQ ID NOs. 25-28, and versions thereof that lack the leader sequence (amino acids 1-26 in any of SEQ ID NOs. 25-28). including VEGF precursors that include all or a part of the signal sequence, or modified forms of VEGF that retain the requisite activities (the ability to bind to a VEGF receptor and internalize a linked targeted agent). Members of the VEGF protein family, including human VEGF121, human VEGF165, human VEGF189, human VEGF206. are preferred. VEGF<sub>121</sub> is particularly preferred. As provided herein VEGF<sub>121</sub> has 10 SEQ ID NO. 25, see, also SEQ ID NOs. 86 and 88 for modified forms, and also is formed from EXONS I-V and VIII (SEQ ID NOs. 16-20 and 24); VEGF165 has SEQ ID NO. 26, see, also SEQ ID NOs. 87 and 89 for modified forms,, and also is formed from EXONS I-V, VII and VIII (SEQ ID NOs. 16-20, 23 and 24); VEGF189 has SEQ ID NO. 27, and also is formed from EXONS I-VII and VIII (SEQ ID NOs. 16-21, 23 and 24); and VEGF206 has SEQ ID NO. 28, and also is formed from EXONS 1-VI, the insert between EXONS VI and VII (see, SEQ ID NO. 22), and EXONS VII and VIII (SEQ ID NOs. 16-24). It is noted that in the sequence of EXON V SEQ ID NO. 2, the second Lys-encoding codon AAG, has been reported as AAA. Consequently, in the VEGF 165, 189, and 206 forms, which contain this codon, the sequence, reported here 20 with the AAG codon, can also be AAA. Molecules, synthetic or naturally occurring, that may be formed from combinations of SEQ ID NOs. 16-24 (or allelic or minor conservatively substituted variations thereof) that possess the ability to bind to a VEGF receptor and internalize a linked targeted agent are intended for use herein. necessary, such combinations of exons may be identified empirically by synthesizing 25 the molecule and testing it, using assays described herein or any other assays known to those of skill in this art, for the ability, either as a monomer, or preferably as a dimer, to bind to a VEGF receptor and internalize a linked targeted agent.

Mutation may be effected by any method known to those of skill in the art. including site-specific or site-directed mutagenesis of DNA encoding the protein and the use of DNA amplification methods using primers to introduce and amplify alterations in the DNA template, such as PCR splicing by overlap extension (SOE). Site-specific mutagenesis is typically effected using a phage vector that has single- and double-stranded forms, such as M13 phage vectors, which are well-known and commercially available. Other suitable vectors that contain a single-stranded phage origin of replication may be used (see, e.g., Veira et al. (1987) Meth. Enzymol. 15:3). In general, site-directed mutagenesis is performed by preparing a single-stranded vector

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that encodes the protein of interest (i.e., a member of the VEGF family or a cytotoxic molecule, such as a saporin). An oligonucleotide primer that contains the desired mutation within a region of homology to the DNA in the single-stranded vector is annealed to the vector followed by addition of a DNA polymerase, such as *E. coli* polymerase I Klenow fragment, which uses the double stranded region as a primer to produce a heteroduplex in which one strand encodes the altered sequence and the other the original sequence. The heteroduplex is introduced into appropriate bacterial cells and clones that include the desired mutation are selected. The resulting altered DNA molecules may be expressed recombinantly in appropriate host cells to produce the modified protein.

The SOE method uses two amplified oligonucleotide products, which have complementary ends as primers and which include an altered codon at the locus at which the mutation is desired, to produce a hybrid product. A second amplification reaction that uses two primers that anneal at the non-overlapping ends amplify the hybrid to produce DNA that has the desired alteration.

In certain embodiments, the heterogeneity of preparations may be reduced by mutagenizing VEGF to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. VEGF is modified by deleting or replacing a site(s) that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of VEGF peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of VEGF or for retention of the ability to bind to a VEGF receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified VEGF is conjugated with a single species of cytotoxic conjugate.

Alternatively, the contribution of each cysteine to the ability to bind to VEGF may be determined empirically. Each cysteine residue may be systematically replaced with a conservative amino acid change (see Table 1, above) or deleted. The resulting mutein is tested for the requisite biological activity: the ability to bind to growth factor receptors and internalize. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. Each of the remaining cysteine residues may be systematically deleted and/or replaced by a serine residue or other residue that would not be expected to alter the structure of the protein. The resulting peptide is tested for biological activity. If the cysteine residue is necessary for

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retention of biological activity it is not deleted; if it not necessary, then it is preferably replaced with a serine or other residue that should not alter the secondary structure of the resulting protein. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a vascular endothelial growth factor receptor and internalize may be determined. It is noted, however, that modified or mutant heparinbinding growth factors may exhibit reduced or no proliferative activity, but may be suitable for use herein, if they retain the ability to target a linked cytotoxic agent to cells bearing receptors to which the unmodified heparin-binding growth factor binds and result in internalization of the cytotoxic moiety. Monomeric forms of VEGF121 contains 9 cysteines and each of VEGF165, VEGF189 and VEGF206 contain 7 additional cysteine residues in the region not present in VEGF121. Any of the 7 are likely to be non-essential for targeting and internalization of linked cytotoxic agents. Recently, the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys-145 in dimerization and biological activity was assessed (Claffery et al., Biochem. Biophys. Acta 1246:1-9, 1995). Dimerization requires Cys-25, Cys-56, and Cys-67. Substitution of any one of these cysteine residues resulted in secretion of a monomeric VEGF, which was inactive in both vascular permeability and endothelial cell mitotic assays. substitution of Cys 145 had no effect on dimerization, although biological activities were somewhat reduced. Substitution of Cys-101 did not result in the production of a secreted or cytoplasmic protein. Thus, substitution of Cys-145 is preferred.

For chemical conjugates, the VEGF monomers are preferably linked via non-essential cysteine residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, preferably the VEGF is dimerized prior to linkage to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

It appears that all of the cysteines that are shared among the four VEGF monomers. VEGF121, VEGF165, VEGF189 and VEGF206 are required. Other cysteines that are present in VEGF165, VEGF189 and VEGF206, that are not present in VEGF121, may be modified, and the resulting modified monomer tested for ability to form dimers and for the requisite biological activities.

In particular, the VEGF molecules exemplified herein (SEQ ID NOs. 25-28) have cysteines at positions 52, 77, 83, 86, 87, 94, 128, and 130 in all VEGF monomers, and elsewhere in all monomers except for VEGF<sub>121</sub>. It appears that the cysteines at residues 77, 86, 87, and 130 are required for intrachain binding and, thus.

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should not be replaced. In order to decrease the potential for aggregate formation, when monomers, other than VEGF<sub>121</sub>, are used it may be desirable to replace the cysteine residues at positions other than 52, 77, 83, 86, 87, 94, 128, and 130, particularly, those in the heparin binding domain in VEGF<sub>165</sub>, VEGF<sub>189</sub> and VEGF<sub>206</sub> may be replaced with a conservative substitution, such as with a serine residue. Any replacements, however, should be checked for retention of the requisite binding and internalization properties. Each cysteine residue may be systematically replaced with a conservative amino acid change or deleted. The resulting mutein is tested for the requisite biological activity, the ability to bind to VEGF receptors and internalize linked targeted moieties. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a VEGF receptor and internalize may be determined.

The VEGF polypeptide may also be modified by addition of one or more cysteine residues at or near the C- or N-terminus, preferably the N-terminus, in order to render it more amenable to chemical conjugation by providing a readily available non-essential cysteine residue. VEGF has been modified herein by addition of Cys residues at or near the N-terminus in order to render them more amenable for chemical conjugation. Any VEGF may be modified for use herein by replacement of one or more cysteine residues that are not required for binding to a VEGF receptor and internalization of the targeted agent. These modified forms of VEGF are particularly suitable for chemical conjugation to linkers and/or targeted agents.

VEGF polypeptides may be isolated by methods known to those of skill in the art or may be prepared by expression of DNA encoding a VEGF protein (see, e.g., Peretz et al. (1992) Biochem. Biophys. Res. Commun. 182:1340-1347; U.S. Patent No. 4,456,550 to Dvorak et al.; U.S. Patent No. 5.219,739 to Tischer et al.; U.S. Patent No. 5,194,596 to Tisher et al.; U.S. Patent No. 5,240,848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications serial nos. 07/351,361, 07/369,424, 07/389,722; to Genentech, Inc., and any U.S. Application Nos. 07/351,361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 Al and EP 0 476 983 Al to Merck & Co.; Houck et al. (1991) Mol. Endo. 5:1806-1814; see also SEQ ID Nos. 18-28 herein). It is understood herein that the key property of any VEGF polypeptide or fragment thereof is the ability, either as monomer or as a dimer, to bind to VEGF receptors and to be internalized by cells bearing such receptors.

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## B. Targeted agents

#### 1. Cytotoxic agents

Cytotoxic agents include any agent that, upon internalization, by a eukaryotic cell.

5 inhibits growth or proliferation of the cell, either by killing the cell or inhibiting a metabolic pathway, transcription, or translation such that cell proliferation slows or stops. Any agent that, when internalized inhibits or destroys cell growth, cell proliferation or other essential cell functions is suitable for use herein. Cytotoxic agents include ribosome inactivating proteins, small metabolic inhibitors, antisense nucleic acids, toxic drugs, such as anticancer agents, and small molecules, such as light activated porphyrins. Ribosome inactivating proteins, such as saporin, are the preferred cytotoxic protein agents for use herein and nucleic acids are the preferred non-peptide agents.

Such cytotoxic agents, include, but are not limited to, saporin, the ricins, abrin and other RIPs, *Pseudomonas* exotoxin, inhibitors of DNA, RNA or protein synthesis, including antisense nucleic acids and other metabolic inhibitors that are known to those of skill in this art. Saporin is preferred, but other suitable RIPs include, but are not limited to, ricin, ricin A chain, maize RIP, gelonin, diphtheria toxin and diphtheria toxin A chain (see, e.g., U.S. Patent No. 4,675,382), trichosanthin, tritin, pokeweed antiviral protein (PAP), mirabilis antiviral protein (MAP), Dianthins 32 and 30, abrin, monordin, bryodin, bryodin2 (PCT application W0 95/11977), shiga, cytotoxically active fragments of cytoxins and others known to those of skill in this art (see, e.g., Barbieri et al. (1982) Cancer Surveys 1:489-520 and European published patent application No. 466,222, incorporated herein by reference, which provide lists of numerous RIPs and their sources; see also, U.S. Patent No. 5,248,608).

The selected cytotoxic agent is, if necessary, derivatized to produce a group reactive with a cysteine on the selected VEGF. If derivatization results in a mixture of reactive species, a mono-derivatized form of the cytotoxic agent can be isolated and then conjugated to the selected VEGF.

### a. Ribosome inactivating proteins

Ribosome-inactivating-proteins (RIPs), which include ricin, abrin and saporin, are plant proteins that catalytically inactivate eukaryotic ribosomes. RIPs inactivate ribosomes by interfering with the protein elongation step of protein synthesis. For example, the RIP saporin (hereinafter also referred to as SAP) has been shown to enzymatically inactivate the 60S ribosome by cleavage of the N-glycosidic bond of the adenine at position 4324 in the rat 28S ribosomal RNA (rRNA). Some RIPs, such as

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the toxins abrin and ricin, contain two constituent chains: a cell-binding chain that mediates binding to cell surface receptors and internalization of the molecule; and an enzymatically active chain responsible for protein synthesis inhibitory activity. Such RIPs are type II RIPs. Other RIPs, such as the saporins, are single chains and are designated type I RIPs. Because such RIPs lack a cell-binding chain, they are far less toxic to whole cells than the RIPs that have two chains.

Several structurally related saporins have been isolated from seeds and leaves of the plant Saponaria officinalis (soapwort). Among these, SAP-6 is the most active and abundant, representing 7% of total seed proteins. Saporin is very stable, has a high isoelectric point, does not contain carbohydrates, and is resistant to denaturing agents, such as sodium dodecyl sulfate (SDS), and a variety of proteases. The amino acid sequences of several saporin-6 isoforms from seeds are known and there appear to be families of saporin RIPs differing in a few amino acid residues. Because saporin is a type I RIP, it does not possess a cell-binding chain. Consequently, its toxicity to whole cells is much lower than the other toxins, such as ricin and abrin. When internalized by eukaryotic cells, however, its cytotoxicity is 100- to 1000-fold more potent than ricin A chain.

Saporin is preferred herein. SO-4 and SO-6 are preferred saporin SAP-6 (also called SO-6) is particularly preferred. The saporin polypeptides include any of the isoforms of saporin that may be isolated from Saponaria officinalis or related species or modified form that retain cytotoxic activity. Such modified forms have amino acid substitutions, deletions, insertions or additions but still express substantial ribosome-inactivating activity. Purified preparations of saporin are frequently observed to include several molecular isoforms of the protein. It is understood that differences in amino acid sequences can occur in saporin from different species as well as between saporin molecules from individual organisms of the same species. In particular, such modified saporin may be produced by modifying the DNA encoding the protein (see, e.g., published International PCT Application WO 93/25688 (Serial No. PCT/US93/05702), United States Application Serial No. 07/901.718; see, also, U.S. Patent Application No. 07/885.242 filed May 20. 1992, and Patent No. 1231914, granted in Italy on January 15, 1992) by altering one or more amino acids or deleting or inserting one or more amino acids, such as a cysteine that may render it easier to conjugate to VEGF or other cell surface binding protein. Any such protein, or portion thereof, that, when conjugated to VEGF as described herein. exhibits cytotoxicity in standard in vitro or in vivo assays within at least about an order of magnitude of the saporin conjugates described herein is contemplated for use herein.

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Thus, the SAP used herein includes any protein that is isolated from natural sources or that is produced by recombinant expression (see, e.g., copending published International PCT Application WO 93/25688 (Serial No. PCT/US93/05702) and United States Application Serial No. 07/901,718, filed June 16, 1992).

Some of the DNA molecules provided herein encode saporin that has substantially the same amino acid sequence and ribosome-inactivating activity as that of saporin-6 (SO-6), including any of four isoforms, which have heterogeneity at amino acid positions 48 and 91 (see, e.g., Maras et al., Biochem. Internat. 21:631-638, 1990, and Barra et al., Biotechnol. Appl. Biochem. 13:48-53, 1991; GB Patent 2,216,891 B and EP Patent 89306106). Other suitable saporin polypeptides include other members of the multi-gene family coding for isoforms of saporin-type ribosome-inactivating proteins including SO-1 and SO-3 (Fordham-Skelton et al., Mol. Gen. Genet. 221:134-138, 1990), SO-2 (see, e.g., U.S. Application Serial No. 07/885,242, which corresponds to GB 2,216,891; see, also, Fordham-Skelton et al., Mol. Gen. Genet. 229:460-466, 1991), SO-4 (see, e.g., GB 2,194,241 B; see, also, Lappi et al., Biochem. Biophys. Res. Commun. 129:934-942, 1985) and SO-5 (see, e.g., GB 2,194,241 B; see, also, Montecucchi et al., Int. J. Peptide Protein Res. 33:263-267, 1989).

# b. Nucleic acids encoding other ribosome-inactivating proteins and cytocides

In addition to saporin discussed above, other cytocides that inhibit protein synthesis are useful in the present invention. The gene sequences for these cytocides may be isolated by standard methods, such as PCR, probe hybridization of genomic or cDNA libraries, antibody screenings of expression libraries, or clones obtained from commercial or other sources. The DNA sequences of many of these cytocides are well known, including ricin A chain (Genbank Accession No. X02388); maize ribosome-inactivating protein (Genbank Accession No. L26305); gelonin (Genbank Accession No. L12243; PCT Application WO 92/03155; U.S. Patent No. 5.376,546; diphtheria toxin (Genbank Accession No. K01722); trichosanthin (Genbank Accession No. M34858); tritin (Genbank Accession No. D13795); pokeweed antiviral protein (Genbank Accession No. X78628); mirabilis antiviral protein (Genbank Accession No. D90347); dianthin 30 (Genbank Accession No. X59260); abrin (Genbank Accession No. X55667); shiga (Genbank Accession No. M19437); and Pseudomonas exotoxin (Genbank Accession Nos. K01397, M23348).

DNA encoding SAP or any cytotoxic agent may be used in the recombinant methods provided herein. In instances in which the cytotoxic agent does not contain a cysteine residue, such as instances in which DNA encoding SAP is

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selected, the DNA may be modified to include a cysteine codon. The codon may be inserted into any locus that does not reduce or reduces by less than about one order of magnitude the cytotoxicity of the resulting protein may be selected. Such locus may be determined empirically by modifying the protein and testing it for cytotoxicity in an assay, such as a cell-free protein synthesis assay. The preferred loci in SAP for insertion of the cysteine residue is at or near the N-terminus (within about 20 residues, preferably 10 residues, of the N-terminus).

#### 2. Expression of cytotoxic agents

Host organisms include those organisms in which recombinant production of heterologous proteins have been carried out and in which the cytotoxic agent, such as saporin is not toxic or of sufficiently low toxicity to permit expression before cell death. Presently preferred host organisms are strains of bacteria. Most preferred host organisms are strains of E. coli, particularly, BL21(DE3) cells (Novagen. Madison, WI).

The DNA encoding the cytotoxic agent, such as saporin protein, is introduced into a plasmid in operative linkage to an appropriate promoter for expression of polypeptides in a selected host organism. The presently preferred saporin proteins are saporin proteins that have been modified by addition of a Cys residue or replacement of a non-essential residue at or near the amino- or carboxyl terminus of the saporin with Cys. Saporin, such as that of SEQ ID No. 7 has been modified by insertion of Met-Cys residue at the N-terminus is preferred. It may additionally be modified by replacement of the Asn or Ile residue at positions 4 and 10, respectively, with cysteine (see Example 4). The DNA fragment encoding the saporin may also include a protein secretion signal that functions in the selected host to direct the mature polypeptide into the periplasm or culture medium. The resulting saporin protein can be purified by methods routinely used in the art, including, methods described hereinafter in the Examples.

Methods of transforming suitable host cells, preferably bacterial cells, and more preferably *E. coli* cells, as well as methods applicable for culturing said cells containing a gene encoding a heterologous protein, are generally known in the art. See, for example, Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

The DNA construct encoding the saporin protein is introduced into the host cell by any suitable means, including, but not limited to transformation employing plasmids, bacterial phage vectors, transfection, electroporation, lipofection, and the like. The heterologous DNA can optionally include sequences, such as origins of

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replication that allow for the extrachromosomal maintenance of the saporin-containing plasmid, or can be designed to integrate into the genome of the host (as an alternative means to ensure stable maintenance in the host).

Positive transformants can be characterized by Southern blot analysis (Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) for the site of DNA integration; Northern blots for inducible-promoter-responsive saporin gene expression; and product analysis for the presence of saporin-containing proteins in either the cytoplasm, periplasm, or the growth media.

Once the saporin-encoding DNA fragment has been introduced into the host cell, the desired saporin-containing protein is produced by subjecting the host cell to conditions under which the promoter is induced, whereby the operatively linked DNA is transcribed. In a preferred embodiment, such conditions are those that induce expression from the *E. coli* lac operon. The plasmid containing the DNA encoding the saporin-containing protein also includes the lac operator region within the promoter and may also include the lac I gene encoding the lac repressor protein (lac18) (see, e.g., Muller-Hill et al. (1968) *Proc. Natl. Acad. Sci. USA* 59:1259-12649). The lac repressor represses the expression from the lac promoter until induced by the addition of IPTG in an amount sufficient to induce transcription of the DNA encoding the saporin-containing protein.

The expression of saporin in *E. coli* is, thus accomplished in a two-stage process. In the first stage, a culture of transformed *E. coli* cells is grown under conditions in which the expression of the saporin-containing protein within the transforming plasmid, preferably encoding a saporin, such as described in Example 4, is repressed by virtue of the lac repressor. In this stage cell density increases. When an optimum density is reached, the second stage commences by addition of IPTG, which prevents binding of repressor to the operator thereby inducing the lac promoter and transcription of the saporin-encoding DNA.

In a preferred embodiment, the promoter is the T7 RNA polymerase promoter, which may be linked to the lac operator and the *E. coli* host strain includes DNA encoding T7 RNA polymerase operably linked to the lac operator and a promoter, preferably the lacUV5 promoter. A preferred plasmid is pET 11a (Novagen, Madison, WI), which contains the T7lac promoter, T7 terminator, the inducible *E. coli* lac operator, and the lac repressor gene. The plasmid pET 15b (Novagen, Madison, WI), which contains a His-Tag<sup>TM</sup> leader sequence (SEQ, ID No. 36) for use in purification with a His column and a thrombin cleavage site that permits cleavage following purification over the column, the T7-lac promoter region and the T7 terminator, has

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been used herein for expression of saporin. Addition of IPTG induces expression of the T7 RNA polymerase and the T7 promoter, which is recognized by the T7 RNA polymerase.

Transformed strains, which are of the desired phenotype and genotype, are grown in fermentors by suitable methods well known in the art. In the first, or growth stage, expression hosts are cultured in defined minimal medium lacking the inducing condition, preferably IPTG. When grown in such conditions, heterologous gene expression is completely repressed, which allows the generation of cell mass in the absence of heterologous protein expression. Subsequent to the period of growth under repression of heterologous gene expression, the inducer, preferably IPTG, is added to the fermentation broth, thereby inducing expression of any DNA operatively linked to an IPTG-responsive promoter (a promoter region that contains lac operator). This last stage is the induction stage.

The resulting saporin-containing protein can be suitably isolated from the other fermentation products by methods routinely used in the art, e.g., using a suitable affinity column as described in the Examples; precipitation with ammonium sulfate; gel filtration; chromatography, preparative flat-bed iso-electric focusing; gel electrophoresis, high performance liquid chromatography (HPLC); and the like. A method for isolating saporin is provided in Example 1 (see, also Lappi et al. ((1985) Biochem. Biophys. Res. Commun., 129:934-942). The expressed saporin protein is isolated from either the cytoplasm, periplasm, or the cell culture medium (see, discussion below and Examples).

#### 3. Porphyrins

Porphyrins are well known light activatable toxins that can be readily cross-linked to proteins (see, e.g., U.S. Patent No. 5,257,970; U.S. Patent No. 5,252,720; U.S. Patent No. 5,238,940; U.S. Patent No. 5,192,788; U.S. Patent No. 5,171,749; U.S. Patent No. 5,149,708; U.S. Patent No. 5,202,317; U.S. Patent No. 5,217,966; U.S. Patent No. 5,053,423; U.S. Patent No. 5,109,016; U.S. Patent No. 5,087,636; U.S. Patent No. 5,028,594; U.S. Patent No. 5,093,349; U.S. Patent No. 4,968,715; U.S. Patent No. 4,920,143 and International Application WO 93/02192).

Porphyrins are conjugated to proteins by direct covalent bonds using. for example, a carbodiimide. Linkage may be effected by treatment of VEGF with 1-ethyl-3-(3-dimethylamino propyl) carbodiimide in the presence of a reaction medium such as DMSO. For other methods see U.S. Patent No. 4.968,715. The porphyrin-VEGF conjugates may be administered topically or systemically. Activation of the

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porphyrin is by irradiating light chosen to match the maximum absorbance of the porphyrin-type photosensitizer.

## 4. Nucleic acids for targeted delivery

The conjugates provided herein are also designed to deliver nucleic acids to targeted cells. The nucleic acids include those intended to deliver a cytotoxic signal to a cell or to modify expression of genes and thereby effect genetic therapy. Examples of nucleic acids include antisense RNA, DNA, ribozymes and oligonucleotides that bind proteins. The nucleic acids can also include RNA trafficking signals, such as viral packaging sequences (see, e.g., Sullenger et al. (1994) Science 262:1566-1569). The nucleic acids also include DNA molecules that encode intact genes or that encode proteins useful for gene therapy or for effecting cell cytotoxicity. Especially of interest are DNA molecules that encode an enzyme that results in cell death or renders a cell susceptible to cell death upon the addition of another product. For example, saporin is an enzyme that cleaves rRNA and inhibits protein synthesis. Other enzymes that inhibit protein synthesis are especially well suited for the present invention. Other enzymes may be used where the enzyme activates a compound with little or no cytotoxicity into a toxic product.

DNA (or RNA) that may be delivered to a cell to effect genetic therapy includes DNA that encodes tumor-specific cytotoxic molecules, such as tumor necrosis factor, viral antigens and other proteins to render a cell susceptible to anti-cancer agents, and DNA encoding genes, such as the defective gene (CFTR) associated with cystic fibrosis (see, e.g., International Application WO 93/03709, which is based on U.S. Application Serial No. 07/745,900; and Riordan et al. (1989) Science 245:1066-1073), to replace defective genes.

Nucleic acids and oligonucleotides for use as described herein can be synthesized by any method known to those of skill in this art (see, e.g., WO 93/01286, which is based on U.S. Application Serial No. 07/723,454; U.S. Patent No. 5,218,088; U.S. Patent No. 5,175,269; U.S. Patent No. 5,109,124). Identification of oligonucleotides and ribozymes for use as antisense agents as well selection of DNA encoding genes for targeted delivery for genetic therapy, as is well within the skill in this art. For example, the desirable properties, lengths and other characteristics of such oligonucleotides are well known. Antisense oligonucleotides are designed to resist degradation by endogenous nucleolytic enzymes and include, but are not limited to: phosphorothioate, methylphosphonate, sulfone, sulfate, ketyl, phosphorodithioate, phosphoramidate, phosphate esters, and other such linkages (see, e.g., Agrwal et al., Tetrehedron Lett. 28:3539-3542 (1987); Miller et al., J. Am. Chem. Soc. 93:6657-6665

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(1971); Stec et al., Tetrehedron Lett. 26:2191-2194 (1985); Moody et al., Nucl. Acids Res. 12:4769-4782 (1989); Uznanski et al., Nucl. Acids Res. (1989); Letsinger et al., Tetrahedron 40:137-143 (1984); Eckstein, Annu. Rev. Biochem. 54:367-402 (1985); Eckstein, Trends Biol. Sci. 14:97-100 (1989); Stein In: Oligodeoxynucleotides.
Antisense Inhibitors of Gene Expression, Cohen, Ed. Macmillan Press, London, pp. 97-117 (1989); Jager et al., Biochemistry 27:7237-7246 (1988)).

#### a. Antisense nucleotides

Antisense nucleotides are oligonucleotides that bind in a sequence-specific manner to nucleic acids, such as mRNA or DNA. When bound to mRNA that has complementary sequences, antisense prevents translation of the mRNA (see, e.g., U.S. Patent No. 5,168,053 to Altman et al.; U.S. Patent No. 5,190,931 to Inouye, U.S. Patent No. 5,135,917 to Burch; U.S. Patent No. 5,087,617 to Smith and Clusel et al. (1993) Nucl. Acids Res. 21:3405-3411, which describes dumbbell antisense oligonucleotides). Triplex molecules refer to single DNA strands that bind duplex DNA forming a colinear triplex molecule and thereby prevent transcription (see, e.g., U.S. Patent No. 5,176,996 to Hogan et al., which describes methods for making synthetic oligonucleotides that bind to target sites on duplex DNA).

Particularly useful antisense nucleotides and triplex molecules are molecules that are complementary or bind to the sense strand of DNA or mRNA that encodes an oncogene, such as bFGF, int-2, hst-1/K-FGF, FGF-5, hst-2/FGF-6, FGF-8. Other useful antisense oligonucleotides include those that are specific for IL-8 (see. e.g., U.S. Patent No. 5,241,049; and International applications WO 89/004836; WO 90/06321; WO 89/10962; WO 90/00563; and WO 91/08483, and the corresponding U.S. applications for descriptions of DNA encoding IL-8 and amino acid sequences of IL-8), which can be linked to bFGF for the treatment of psoriasis, anti-sense oligonucleotides that are specific for nonmuscle myosin heavy chain and/or c-myb (see. e.g., Simons et al. (1992) Circ. Res. 70:835-843; WO 93/01286, which is based on U.S. application Serial No. 07/723,454: LeClerc et al. (1991) J. Am. Coll. Cardiol. 17 (2 Suppl. A):105A; Ebbecke et al. (1992) Basic Res. Cardiol. 87:585-591), which can be targeted by an FGF to inhibit smooth muscle cell proliferation. such as that following angioplasty and thereby prevent restenosis or inhibit viral gene expression in transformed or infected cells.

#### b. Ribozymes

A ribozyme is an RNA molecule that specifically cleaves RNA substrates, such mRNA, and thus inhibit or interfere with cell growth or expression.

There are at least five classes of ribozymes that are known that are involved in the cleavage and/or ligation of RNA chains. Ribozymes can be targeted to any RNA transcript and can catalytically cleave such transcript (see, e.g., U.S. Patent No. 5,272,262; U.S. Patent No. 5,144,019; and U.S. Patent Nos. 5,168,053, 5.180,818, 5,116,742 and 5,093,246 to Cech et al., which described ribozymes and methods for production thereof). Any such ribosome may be linked to the growth factor for delivery to VEGF-receptor bearing cells.

The ribozymes may be delivered to the targeted cells, such tumor cells that express a receptor to which VEGF binds and upon binding is internalized, as DNA encoding the ribozyme linked to a eukaryotic promoter, such as a eukaryotic viral promoter, generally a late promoter, such that upon introduction into the nucleus, the ribozyme will be directly transcribed. In such instances, the construct will also include a nuclear translocation sequence (NTS; see Table 2, below), generally as part of the growth factor or as part of a linker between the growth factor and linked DNA.

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#### c. Nucleic acids encoding therapeutic products

Among the DNA that encodes therapeutic products contemplated for use is DNA encoding correct copies of defective genes, such as the defective gene (CFTR) associated with cystic fibrosis (see, e.g., International Application WO 93/03709, which is based on U.S. Application Serial No. 07/745,900; and Riordan et al. (1989) Science 245:1066-1073), and anticancer agents, such as tumor necrosis factors, and cytotoxic agents, such as saporin to VEGF-receptor bearing cells. The conjugate should include an NTS. If the conjugate is designed such that the VEGF and linked DNA is cleaved in the cytoplasm, then the NTS should be included in a portion of the linker that remains bound to the DNA, so that, upon internalization, the conjugate will be trafficked to the nucleus. The nuclear translocation sequence (NTS) may be a heterologous sequence or a may be derived from the selected growth factor.

#### d. Other nucleic acids

30 Extracellular protein binding oligonucleotides refer to oligonucleotides

that specifically bind to proteins. Small nucleotide molecules refer to nucleic acids that target a receptor site.

#### Coupling of nucleic acids to proteins

To effect chemical conjugation herein, the VEGF protein is linked to the nucleic acid either directly or via one or more linkers. Methods for conjugating nucleic acids, at the 5' ends, 3' ends and elsewhere, to the amino and carboxyl termini and other

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sites in proteins are known to those of skill in the art (for a review see e.g., Goodchild, (1993) In: Perspectives in Bioconjugate Chemistry, Mears, Ed., American Chemical Society, Washington, D.C. pp. 77-99). For example, proteins have been linked to nucleic acids using ultraviolet irradiation (Sperling et al. (1978) Nucleic Acids Res. 5:2755-2773; Fiser et al. (1975) FEBS Lett. 52:281-283), bifunctional chemicals (Bäumert et al. (1978) Eur. J. Biochem. 89:353-359; and Oste et al. (1979) Mol. Gen. Genet. 168:81-86) photochemical cross-linking (Vanin et al. (1981) FEBS Lett. 124:89-92; Rinke et al. (1980) J.Mol.Biol. 137:301-314; Millon et al. (1980); Eur. J. Biochem. 110:485-454).

In particular, the reagents (N-acetyl-N'-(p-glyoxylylbenzolyl) cystamine and 2-iminothiolane have been used to couple DNA to proteins, such as  $\alpha$  2macroglobulin ( $\alpha$ 2M) via mixed disulfide formation (see, Cheng et al. (1983) *Nucleic Acids Res.* 11:659-669). N-acetyl-N'-(p-glyoxylylbenzolyl)cystamine reacts specifically with nonpaired guanine residues and, upon reduction, generates a free sulfhydryl group. 2-Iminothiolane reacts with proteins to generate sulfhydryl groups that are then conjugated to the derivatized DNA by an intermolecular disulfide interchange reaction. Any linkage may be used provided that, upon internalization of the conjugate the targeted nucleic acid is active. Thus, it is expected that cleavage of the linkage may be necessary, although it is contemplated that for some reagents, such as DNA encoding ribozymes linked to promoters or DNA encoding therapeutic agents for delivery to the nucleus, such cleavage may not be necessary.

Thiol linkages can be readily formed using heterbiofunctional reagents. Amines have also been attached to the terminal 5' phosphate of unprotected oligonucleotides or nucleic acids in aqueous solutions by reacting the nucleic acid with a water-soluble carbodiimide, such as 1-ethyl-3'[3-dimethylaminopropyl]carbodiimide (EDC) or N-ethyl-N'(3-dimethylaminopropylcarbodiimidehydrochloride (EDCI), in imidazole buffer at pH 6 to produce the 5'phosphorimidazolide. Contacting the 5'phosphorimidazolide with amine-containing molecules, such as a VEGF, and ethylenediamine, results in stable phosphoramidates (see, e.g., Chu et al. (1983) Nucleic Acids Res. 11:6513-6529; and WO 88/05077). In particular, a solution of DNA is saturated with EDC, at pH 6 and incubated with agitation at 4°C overnight. The resulting solution is then buffered to pH 8.5 by adding, for example about 3 volutes of 100 mM citrate buffer, and adding about 5 µg - about 20 µg of a VEGF, and agitating the resulting mixture at 4°C for about 48 hours. The unreacted protein may be removed from the mixture by column chromatography using, for example, Sephadex G75 (Pharmacia) using 0.1 M ammonium carbonate solution, pH 7.0 as an eluting buffer. The isolated conjugate may be lyophilized and stored until used.

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U.S. Patent No. 5.237,016 provides methods for preparing nucleotides that are bromacetylated at their 5' termini and reacting the resulting oligonucleotides with thiol groups. Oligonucleotides derivatized at their 5'-termini bromoacetyl groups can be prepared by reacting 5'-aminohexyl-phosphoramidate oligonucleotides with bromoacetic acid-N-hydroxysuccinimide ester as described in U.S. Patent No. 5,237,016. U.S. Patent No. 5,237,016 also describes methods for preparing thiolderivatized nucleotides, which can then be reacted with thiol groups on the selected growth factor. Briefly, thiol-derivatized nucleotides are prepared using a 5'-phosphorylated nucleotide in two steps: (1) reaction of the phosphate group with imidazole in the presence of a diimide and displacement of the imidazole leaving group with cystamine in one reaction step; and reduction of the disulfide bond of the cystamine linker with dithiothreitol (see, also, Orgel et al. ((1986) Nucl. Acids Res. 14:651, which describes a similar procedure). The 5'-phosphorylated starting oligonucleotides can be prepared by methods known to those of skill in the art (see, e.g., Maniatis et al. (1982) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, New York, p. 122).

The antisense oligomer or nucleic acid, such as a methylphosphonate oligonucleotide (MP-oligomer), may be derivatized by reaction with SPDP or SMPB. The resulting MP-oligomer may be purified by HPLC and then coupled to VEGF, which may be modified replacement of one or more non-essential cysteine residues, as described above. The MP-oligomer (about 0.1  $\mu$ M) is dissolved in about 40-50  $\mu$ l of 1:1 acetonitrile/water to which phosphate buffer (pH 7.5, final concentration 0.1 M) and a 1 mg MP-oligomer in about 1 ml phosphate buffered saline is added. The reaction is allowed to proceed for about 5-10 hours at room temperature and is then quenched with about 15  $\mu$ L 0.1 iodoacetamide. The VEGF-oligonucleotide conjugates can be purified on heparin sepharose Hi-Trap columns (1 ml, Pharmacia) and eluted with a linear or step gradient. The conjugate should elute in 0.6 M NaCl.

#### f. Nucleic acids encoding cytocides

A cytocide-encoding agent is a nucleic acid molecule (DNA or RNA) that, upon internalization by a cell, and subsequent transcription and/or translation into a cytocidal agent, is cytotoxic to a cell or inhibits cell growth by inhibiting protein synthesis.

Cytocides include saporin, the ricins, abrin and other ribosome-35 inactivating proteins, *Pseudomonas* exotoxin, diptheria toxin, angiogenin, tritin, dianthins 32 and 30, momordin, pokeweed antiviral protein, mirabilis antiviral protein.

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bryodin, angiogenin, and shiga exotoxin, as well as other cytocides that are known to those of skill in the art.

Especially of interest are DNA molecules that encode an enzyme that results in cell death or renders a cell susceptible to cell death upon the addition of another product. For example, saporin, a preferred cytocide, is an enzyme that cleaves rRNA and inhibits protein synthesis. Other enzymes that inhibit protein synthesis are especially well suited for use in the present invention. In addition, enzymes may be used where the enzyme activates a compound with little or no cytotoxicity into a toxic product that inhibits protein synthesis.

In addition to saporin discussed above, other cytocides that inhibit protein synthesis are useful in the present invention. The gene sequences for these cytocides may be isolated by standard methods, such as PCR, probe hybridization of genomic or cDNA libraries, antibody screenings of expression libraries, or obtain clones from commercial or other sources. The DNA sequences of many of these cytocides are well known, including ricin A chain (Genbank Accession No. X02388); maize ribosome-inactivating protein (Genbank Accession No. L26305); gelonin (Genbank Accession No. L12243; PCT Application WO 92/03155; U.S. Patent No. 5,376,546; diphtheria toxin (Genbank Accession No. K01722); trichosanthin (Genbank Accession No. M34858); tritin (Genbank Accession No. D13795); pokeweed antiviral protein (Genbank Accession No. X78628); mirabilis antiviral protein (Genbank Accession No. D90347); dianthin 30 (Genbank Accession No. X59260); abrin (Genbank Accession No. X55667); shiga (Genbank Accession No. M19437) and Pseudomonas exotoxin (Genbank Accession Nos. K01397, M23348).

In the case of cytotocide molecules such as the ribosome-inactivating proteins, very few molecules may need be present for cell killing. Indeed, only a single molecule of diphtheria toxoid introduced into a cell was sufficient to kill the cell. In other cases, it may be that propagation or stable maintenance of the construct is necessary to attain sufficient numbers or concentrations of the gene product for effective gene therapy. Examples of replicating and stable eukaryotic plasmids are found in the scientific literature.

In general, constructs will also contain elements necessary for transcription and translation. If the cytocide-encoding agent is DNA, then it must contain a promoter. The choice of the promoter will depend upon the cell type to be transformed and the degree or type of control desired. Promoters can be constitutive or active in any cell type, tissue specific, cell specific, event specific or inducible. Cell-type specific promoters and event type specific promoters are preferred. Examples of constitutive or nonspecific promoters include the SV40 early promoter (U.S. Patent No.

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5,118,627), the SV40 late promoter (U.S. Patent No. 5,118,627), CMV early gene promoter (U.S. Patent No. 5,168,062), and adenovirus promoter. In addition to viral promoters, cellular promoters are also amenable within the context of this invention. In particular, cellular promoters for the so-called housekeeping genes are useful. Viral promoters are preferred, because generally they are stronger promoters than cellular promoters.

Tissue specific promoters are particularly useful when a particular tissue type is to be targeted for transformation. By using one of this class of promoters, an extra margin of specificity can be attained. For example, when the indication to be treated is ophthalmological, either the alpha-crystalline promoter or gamma-crystalline promoter is preferred. When a tumor is the target of gene delivery, cellular promoters for specific tumor markers or promoters more active in tumor cells should be chosen. Thus, to transform prostate tumor cells the prostate-specific antigen promoter is especially useful. Similarly, the tyrosinase promoter or tyrosinase-related protein promoter is a preferred promoter for melanoma treatment. For B lymphocytes, the immunoglobulin variable region gene promoter, for T lymphocytes, the TCR receptor variable region promoter, for helper T lymphocytes, the CD4 promoter, for liver, the albumin promoter, are but a few examples of tissue specific promoters. Many other examples of tissue specific promoters are readily available to one skilled in the art.

Inducible promoters may also be used. These promoters include the MMTV LTR (PCT WO 91/13160), which is inducible by dexamethasone, metallothionein, which is inducible by heavy metals, and promoters with cAMP response elements, which are inducible by cAMP. By using an inducible promoter, the nucleic acid may be delivered to a cell and will remain quiescent until the addition of the inducer. This allows further control on the timing of production of the therapeutic gene.

Event-type specific promoters are active only upon the occurrence of an event, such as tumorigenecity or viral infection. The HIV LTR is a well known example of an event-specific promoter. The promoter is inactive unless the *tat* gene product is present, which occurs upon viral infection.

Additionally, promoters that are coordinately regulated with a particular cellular gene may be used. For example, promoters of genes that are coordinately expressed when a particular VEGF receptor gene is expressed may be used. Then, the nucleic acid will be transcribed when the VEGF receptor, such as VEGFR1, is expressed, and not when VEGFR2 is expressed. This type of promoter is especially useful when one knows the pattern of VEGF receptor expression in a particular tissue.

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so that specific cells within that tissue may be killed upon transcription of a cytotoxic agent gene without affecting the surrounding tissues.

Alternatively, cytocide gene products may be noncytotoxic but activate a compound, which is endogenously produced or exogenously applied, from a nontoxic form to a toxic product that inhibits protein synthesis.

The construct must contain the sequence that binds to the nucleic acid binding domain, if the domain binds in a sequence specific manner. As described below, the target nucleotide sequence may be contained within the coding region of the cytocide, in which case, no additional sequence need be incorporated. It may be desirable to have multiple copies of target sequence. If the target sequence is coding sequence, the additional copies must be located in non-coding regions of the cytocide-encoding agent. The target sequences of the nucleic acid binding domains are typically generally known. The target sequence may be readily determined, in any case. Techniques are generally available for establishing the target sequence (e.g., see PCT Application WO 92/05285 and U.S. Serial No. 586,769).

Specificity of delivery is achieved by coupling a nucleic acid binding domain to a receptor-binding internalized ligand, either by chemical conjugation or by constructing a fusion protein. Linkers as described above may be used. The receptor-binding internalized ligand part confers specificity of delivery in a cell-specific manner. The choice of the receptor-binding internalized ligand to use will depend upon the receptor expressed by the target cells. The receptor type of the target cell population may be determined by conventional techniques such as antibody staining, PCR of cDNA using receptor-specific primers, and biochemical or functional receptor binding assays. It is preferable that the receptor be cell type specific or have increased expression or activity (i.e., higher rate of internalization) within the target cell population.

The nucleic acid binding domain can be of two types, non-specific in its ability to bind nucleic acid, or highly specific so that the amino acid residues bind only the desired nucleic acid sequence. Nonspecific binding proteins, polypeptides, or compounds are generally polycations or highly basic. Lys and Arg are the most basic of the 20 common amino acids; proteins enriched for these residues are candidates for nucleic acid binding domains. Examples of basic proteins include histones, protamines, and repeating units of lysine and arginine. Poly-L-lysine is a well-used nucleic acid binding domain (see U.S. Patent Nos. 5.166.320 and 5.354.844). Other polycations, such as spermine and spermidine, may also be used to bind nucleic acids. By way of example, the sequence-specific proteins including Sp-1, AP-1, myoD and the rev gene product from HIV may be used. Specific nucleic acid binding domains can be cloned

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in tandem, individually, or multiply to a desired region of the receptor-binding internalized ligand of interest. Alternatively, the domains can be chemically conjugated to each other.

The corresponding response elements that bind sequence-specific domains are incorporated into the construct to be delivered. Complexing the cytocidal-encoding agent to the receptor-binding internalized ligand/nucleic acid binding domain allows specific binding of response element to the nucleic acid binding domain. Even greater specificity of binding may be achieved by identifying and using the minimal amino acid sequence that binds to the cytocidal-encoding agent of interest. For example, phage display methods can be used to identify amino acids residues of varying length that will bind to specific nucleic acid sequences with high affinity. (See U.S. Patent No. 5,223,409.) The peptide sequence can then be cloned into the receptor-binding internalized ligand as a single copy or multiple copies. Alternatively, the peptide may be chemically conjugated to the receptor-binding internalized ligand. Incubation of the cytocide-encoding agent with the conjugated proteins will result in a specific binding between the two.

These complexes may be used to deliver nucleic acids that encode saporin or other cytocidal proteins into cells that have appropriate receptors that are expressed, over-expressed or more active in internalization upon binding. The cytocide gene is cloned downstream of a mammalian promoter such as SV40, CMV, TK or Adenovirus promoter. As described above, promoters of interest may be active in an cell type, active only in a tissue-specific manner, such as  $\alpha$ -crystalline or tyrosinase, event specific or inducible, such as the MMTV LTR.

Receptor-binding internalized ligands are prepared as discussed by any suitable method, including recombinant DNA technology, isolation from a suitable source, purchase from a commercial source, or chemical synthesis. The selected linker or linkers is (are) linked to the receptor-binding internalized ligands by chemical reaction, generally relying on an available thiol or amine group on the receptor-binding internalized ligands. Heterobifunctional linkers are particularly suited for chemical conjugation. Alternatively, if the linker is a peptide linker, then the receptor-binding internalized ligands, linker and nucleic acid binding domain can be expressed recombinantly as a fusion protein.

VEGF may be isolated from a suitable source or may be produced using recombinant DNA methodology, discussed below. To effect chemical conjugation herein, the growth factor protein is conjugated generally via a reactive amine group or thiol group to the nucleic acid binding domain directly or through a linker to the nucleic acid binding domain. The growth factor protein is conjugated either via its N-terminus.

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C-terminus, or elsewhere in the polypeptide. In preferred embodiments, the growth factor protein is conjugated via a reactive cysteine residue to the linker or to the nucleic acid binding domain. The growth factor can also be modified by addition of a cysteine residue, either by replacing a residue or by inserting the cysteine, at or near the amino or carboxyl terminus, within about 20, preferably 10 residues from either end, and preferably at or near the amino terminus.

In certain embodiments, the heterogeneity of preparations may be reduced by mutagenizing the growth factor protein to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. The growth factor protein is modified by deleting or replacing a site(s) on the growth factor that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of heparin-binding growth factor peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of the growth factor or for retention of the ability to bind to a growth factor receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified heparin-binding growth factor is conjugated with a single species of cytotoxic conjugate.

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Alternatively, the contribution of each cysteine to the ability to bind to VEGF receptors may be determined empirically. Each cysteine residue may be systematically replaced with a conservative amino acid change (see Table 1, above) or deleted. The resulting mutein is tested for the requisite biological activity: the ability to bind to growth factor receptors and internalize linked nucleic acid binding domain and agents. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. Each of the remaining cysteine residues may be systematically deleted and/or replaced by a serine residue or other residue that would not be expected to alter the structure of the protein. The resulting peptide is tested for biological activity. If the cysteine residue is necessary for retention of biological activity it is not deleted; if it not necessary, then it is preferably replaced with a serine or other residue that should not alter the secondary structure of the resulting protein. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a heparin-binding growth factor receptor and internalize may be determined. It is noted. however, that modified or mutant heparin-binding growth factors may exhibit reduced or no proliferative activity, but may be suitable for use herein, if they retain the ability

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to target a linked cytotoxic agent to cells bearing receptors to which the unmodified heparin-binding growth factor binds and result in internalization of the cytotoxic moiety. In the case of monomeric VEGF, VEGF121 contains 9 cysteines and each of VEGF165, VEGF189 and VEGF206 contain 7 additional residues in the region not present in VEGF121. Any of the 7 are likely to be non-essential for targeting and internalization of linked cytotoxic agents. Recently, the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys-145 in dimerization and biological activity was assessed (Claffery et al., *Biochem. Biophys. Acta 1246*:1-9, 1995). Dimerization requires Cys-25, Cys-56, and Cys-67. Substitution of any one of these cysteine residues resulted in secretion of a monomeric VEGF, which was inactive in both vascular permeability and endothelial cell mitotic assays. In contrast, substitution of Cys 145 had no effect on dimerization, although biological activities were somewhat reduced. Substitution of Cys-101 did not result in the production of a secreted or cytoplasmic protein. Thus, substitution of Cys-145 is preferred.

The VEGF monomers are preferably linked via non-essential cysteine residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, preferably the VEGF is dimerized prior to linkage to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

Methods for chemical conjugation of proteins are known to those of skill in the art. The preferred methods for chemical conjugation depend on the selected components, but preferably rely on disulfide bond formation. For example, if the targeted agent is SPDP-derivatized saporin, then it is advantageous to dimerize the VEGF moiety prior coupling or conjugating to the derivatized saporin. If VEGF is modified to include a cysteine residue at or near the N-, preferably, or C- terminus, then dimerization should follow coupling to the nucleic acid binding domain. To effect chemical conjugation herein, the VEGF polypeptide is linked via one or more selected linkers or directly to the nucleic acid binding domain.

A nucleic acid binding domain is prepared for chemical conjugation. For chemical conjugation, a nucleic acid binding domain may be derivatized with SPDP or other suitable chemicals. If the binding domain does not have a Cys residue available for reaction, one can be either inserted or substituted for another amino acid. If desired, mono-derivatized species may be isolated, essentially as described.

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For chemical conjugation, the nucleic acid binding domain may be derivatized or modified such that it includes a cysteine residue for conjugation to the receptor-binding internalized ligand. Typically, derivatization proceeds by reaction with SPDP. This results in a heterogeneous population. For example, nucleic acid binding domain that is derivatized by SPDP to a level of 0.9 moles pyridine-disulfide per mole of nucleic acid binding domain includes a population of non-derivatized, mono-derivatized and di-derivatized SAP. nucleic acid binding domain proteins, which are overly derivatized with SPDP, may lose ability to bind nucleic acid because of reaction with sensitive lysines (Lambert et al., Cancer Treat. Res. 37:175-209, 1988). The quantity of non-derivatized nucleic acid binding domain in the preparation of the non-purified material can be difficult to judge and this may lead to errors in being able to estimate the correct proportion of derivatized nucleic acid binding domain to add to the reaction mixture.

Because of the removal of a negative charge by the reaction of SPDP with lysine, the three species, however, have a charge difference. The methods herein rely on this charge difference for purification of mono-derivatized nucleic acid binding domain by Mono-S cation exchange chromatography. The use of purified mono-derivatized nucleic acid binding domain has distinct advantages over the non-purified material. The amount of receptor-binding internalized ligand that can react with nucleic acid binding domain is limited to one molecule with the mono-derivatized material, and it is seen in the results presented herein that a more homogeneous conjugate is produced. There may still be sources of heterogeneity with the mono-derivatized nucleic acid binding domain used here but is acceptable as long as binding to the cytocide-encoding agent is not impacted.

Because more than one amino group on the nucleic acid binding domain may react with the succinimidyl moiety, it is possible that more than one amino group on the surface of the protein is reactive. This creates potential for heterogeneity in the mono-derivatized nucleic acid binding domain. As an alternative to derivatizing to introduce a sulfhydryl, the nucleic acid binding domain can be modified by the introduction of a cysteine residue. Preferred loci for introduction of a cysteine residue include the N-terminus region, preferably within about one to twenty residues from the N-terminus of the nucleic acid binding domain. Using either methodology (reacting mono-derivatized nucleic acid binding domain introducing a Cys residue into nucleic acid binding domain), the resulting preparations of chemical conjugates are monogenous; compositions containing the conjugates also appear to be free of aggregates. As a preferred alternative, heterogeneity can be avoided by producing a

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fusion protein of receptor-binding internalized ligand and nucleic acid binding domain, as described below.

Expression of DNA encoding a fusion of a receptor-binding internalized ligand polypeptide linked to the nucleic acid binding domain results in a more homogeneous preparation of cytotoxic conjugates. Aggregate formation can be reduced in preparations containing the fusion proteins by modifying the receptor-binding internalized ligand, such as by removal of nonessential cysteines, and/or the nucleic acid binding domain to prevent interactions between conjugates via free cysteines.

DNA encoding the polypeptides may be isolated, synthesized or obtained from commercial sources or prepared as described herein. Expression of recombinant polypeptides may be performed as described herein; and DNA encoding these polypeptides may be used as the starting materials for the methods herein.

As described above, DNA encoding VEGF are described above. DNA may be prepared synthetically based on the amino acid or DNA sequence or may be isolated using methods known to those of skill in the art, such as PCR, probe hybridization of libraries, and the like or obtained from commercial or other sources.

As described herein, such DNA may then be mutagenized using standard methodologies to delete or replace any cysteine residues that are responsible for aggregate formation. If necessary, the identity of cysteine residues that contribute to aggregate formation may be determined empirically, by deleting and/or replacing a cysteine residue and ascertaining whether the resulting growth factor with the deleted cysteine forms aggregates in solutions containing physiologically acceptable buffers and salts. Loci for insertion of cysteine residues may also be determined empirically. Generally, regions at or near (within 20, preferably 10 amino acids) the C- or, preferably, the N-terminus are preferred.

The DNA construct encoding the fusion protein can be inserted into a plasmid and expressed in a selected host, as described above, to produce a recombinant receptor-binding internalized ligand—nucleic acid binding domain conjugate. Multiple copies of the chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will then be a multimer. Typically, two to six copies of the chimera are inserted, preferably in a head to tail fashion, into one plasmid.

To produce monogenous preparations of fusion protein, DNA VEGF is modified so that, upon expression, the resulting VEGF portion of the fusion protein does not include any cysteines available for reaction. In preferred embodiments, DNA encoding an VEGF polypeptide is linked to DNA encoding a nucleic acid binding domain. The DNA encoding the VEGF polypeptide or other receptor-binding

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internalized ligand is modified in order to remove the translation stop codon and other transcriptional or translational stop signals that may be present and to remove or replace DNA encoding the available cysteines. The DNA is then ligated to the DNA encoding the nucleic acid binding domain polypeptide directly or via a linker region of one or more codons between the first codon of the nucleic acid binding domain and the last codon of the VEGF. The size of the linker region may be any length as long as the resulting conjugate binds and is internalized by a target cell. Presently, spacer regions of from about one to about seventy-five to ninety codons are preferred. The order of the receptor-binding internalized ligand and nucleic acid binding domain in the fusion protein may be reversed. If the nucleic acid binding domain is N-terminal, then it is modified to remove the stop codon and any stop signals.

If the VEGF or other ligand has been modified so as to lack mitogenic activity or other biological activities, binding and internalization may still be readily assayed by any one of the following tests or other equivalent tests. Generally, these tests involve labeling the ligand, incubating it with target cells, and visualizing or measuring intracellular label. For example, briefly, VEGF may be fluorescently labeled with FITC or radiolabeled with <sup>125</sup>I. Fluorescein-conjugated VEGF is incubated with cells and examined microscopically by fluorescence microscopy or confocal microscopy for internalization. When VEGF is labeled with <sup>125</sup>I, the labeled VEGF is incubated with cells at 4°C. Cells are temperature shifted to 37°C and washed with 2 M NaCl at low pH to remove any cell-bound VEGF. Label is then counted and thereby measuring internalization of VEGF. Alternatively, the ligand can be conjugated with an nucleic acid binding domain by any of the methods described herein and complexed with a plasmid encoding saporin. As discussed below, the complex may be used to transfect cells and cytoxicity measured.

The DNA encoding the resulting receptor-binding internalized ligandnucleic acid binding domain can be inserted into a plasmid and expressed in a selected host, as described above, to produce a monogenous preparation.

Multiple copies of the modified receptor-binding internalized ligand/nucleic acid binding domain chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will be a multimer. Typically two to six copies of the chimera are inserted, preferably in a head to tail fashion, into one plasmid. Merely by way of example, DNA encoding human bFGF- has been mutagenized using splicing by overlap extension (SOE). Each application of the SOE method uses two amplified oligonucleotide products, which have complementary ends as primers and which include an altered codon at the locus at which the mutation is desired, to produce a hybrid product. A second amplification

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reaction that uses two primers that anneal at the non-overlapping ends amplify the hybrid to produce DNA that has the desired alteration.

The receptor-binding internalized ligand/nucleic acid binding domain is incubated with the cytocide-encoding agent, typically a DNA molecule, to be delivered under conditions that allow binding of the nucleic acid binding domain to the agent. Conditions will vary somewhat depending on the nature of the nucleic acid binding domain, but will typically occur in 0.1M NaCl and 20 mM HEPES or other similar buffer.

The desired application is the delivery of cytotocidal agents, such as saporin, in a non-toxic form. By delivering a nucleic acid molecule capable of expressing saporin, the timing of cytotoxicity may be exquisitely controlled. For example, if saporin is expressed under the control of a tissue-specific promoter, then uptake of the complex by cells having the tissue-specific factors necessary for promoter activation will result in the killing of those cells. On the other hand, if cells taking up the complex do not have those tissue-specific factors, the cells will be spared.

Merely by way of example, test constructs have been made and tested. One construct is a chemical conjugate of bFGF and poly-L-lysine. The bFGF molecule is a variant in which the Cys residue at position 96 has been changed to a serine; thus, only the Cys at position 78 is available for conjugation. This bFGF is called VEGF2-3. The poly-L-lysine was derivatized with SPDP and coupled to FGF2-3. This FGF2-3/poly-L-lysine conjugate was used to deliver a plasmid able to express the  $\beta$ -galactosidase gene.

The ability of a construct to bind nucleic acid molecules may be conveniently assessed by agarose gel electrophoresis. Briefly, a plasmid, such as  $pSV\beta$ , is digested with restriction enzymes to yield a variety of fragment sizes. For ease of 25 detection, the fragments may be labeled with <sup>32</sup>P either by filling in of the ends with DNA polymerase I or by phosphorylation of the 5'-end with polynucleotide kinase following dephosphorylation by alkaline phosphatase. The plasmid fragments are then incubated with the receptor-binding internalized ligand/nucleic acid binding domain in this case. FGF2-3/poly-L-lysine in a buffered saline solution, such as 20 mM HEPES. pH 7.3, 0.1M NaCl. The reaction mixture is electrophoresed on an agarose gel alongside similarly digested, but nonreacted fragments. If a radioactive label was incorporated, the gel may be dried and autoradiographed. If no radioactive label is present, the gel may be stained with ethidium bromide and the DNA visualized through appropriate red filters after excitation with UV. Binding has occurred if the mobility of 35 the fragments is retarded compared to the control. In the example case, the mobility of the fragments was retarded after binding with the FGF2-3/poly-L-lysine conjugate.

Further testing of the conjugate is performed to show that it binds to the cell surface receptor and is internalized into the cell. It is not necessary that the receptor-binding internalized ligand part of the conjugate retain complete biological activity. For example, VEGF is mitogenic on certain cell types. As discussed above, this activity may not always be desirable. If this activity is present, a proliferation assay is performed. Likewise, for each desirable activity, an appropriate assay may be performed. However, for application of the subject invention, the only criteria that need be met are receptor binding and internalization.

Receptor binding and internalization may be measured by the following three assays. (1) A competitive inhibition assay of the complex to cells expressing the 10 appropriate receptor demonstrates receptor binding. (2) Receptor binding and internalization may be assayed by measuring β-gal expression (e.g., enzymatic activity) in cells that have been transformed with a complex of a \beta-gal containing plasmid condensed with a receptor-binding internalized ligand/nucleic acid binding domain. This assay is particularly useful for optimizing conditions to give maximal 15 transformation. Thus, the optimum ratio of receptor-binding internalized ligand/nucleic acid binding domain to nucleic acid and the amount of DNA per cell may readily be determined by assaying and comparing the enzymatic activity of \beta-gal. As such, these first two assays are useful for preliminary analysis and failure to show receptor binding or β-gal activity does not per se eliminate a candidate receptor-binding internalized 20 ligand/nucleic acid binding domain conjugate or fusion protein from further analysis. (3) The preferred assay is a cytotoxicity assay performed on cells transformed with a cytocide-encoding agent bound by receptor-binding internalized ligand/nucleic acid binding domain. While, in general, any cytocidal molecule may be used, ribosome-25 inactivating proteins are preferred and saporin, or another type I ribosome-inactivating protein, is particularly preferred. A statistically significant reduction in cell number demonstrates the ability of the receptor-binding internalized ligand/nucleic acid binding domain conjugate or fusion to deliver nucleic acids into a cell.

### 30 C. Other elements

### 1. Nuclear translocation signals

As used herein, a nuclear translocation or targeting sequence (NTS) is a sequence of amino acids in a protein that are required for translocation of the protein into a cell nucleus. Examples of NTS are set forth in Table 2, below. Comparison with known NTSs, and if necessary testing of candidate sequences, should permit those of skill in the art to readily identify other amino acid sequences that function as NTSs.

As used herein, heterologous NTS refers to an NTS that is different from the NTS that occurs in the wild-type peptide, polypeptide, or protein. For example, the NTS may be derived from another polypeptide, it may be synthesized, or it may be derived from another region in the same polypeptide. A typical consensus NTS sequence contains an amino-terminal proline or glycine followed by at least three basic residues in a array of seven to nine amino acids (see, e.g. Dang et al. (1989) J. Biol. Chem. 264:18019-18023, Dang et al. (1988) Mol. Cell. Biol. 8:4049-4058 and Table 2, which sets forth examples of NTSs and regions of proteins that share homology with known NTSs),

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TABLE 2

SV40 large T         Pro126LysLysArgLysValGlu         90           Polyoma large T         Pro279 ProLysLysAlaArgGluVal         91           Human c-Myc         Pro120 AlaAlaLysArgValLysLeuAsp         92           Adenovirus E1A         Lys281 ArgProArgPro         93           Yeast mat α2         Lys31leProIleLys         94           C-Erb-A         B. Ser127 LysArgLysArgLysSer         95           c-Erb-A         B. Ser127 LysArgValAlaLysArgLysleu         96           C. Ser181 HisTrpLysGlnLysArgLysPhe         97           c-Myb         Pro221 LeuLeuLysLysIleLysGln         98           p53         Pro316 GlnProLysLysLysIleLysGln         98           p53         Pro277 GlyLysArgLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly48 ArgLysLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly48 ArgLysLysLysProLysLeu         102           FGF-1         AsnTyrLysLysProLysLeu         102           FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgClnArgArg         76 <th></th> <th></th> <th></th>			
Polyoma large T         Pro <sup>279</sup> ProLysLysAlaArgGluVal         91           Human c-Myc         Pro <sup>120</sup> AlaAlaLysArgValLysLeuAsp         92           Adenovirus E1A         Lys²81 ArgProArgPro         93           Yeast mat α2         Lys³1leProlleLys         94           α. Gly²²LysArgLysArgLysSer         95           c-Erb-A         B. Ser¹²² LysArgValAlaLysArgLysleu         96           C. Ser¹81 HisTrpLysGlnLysArgLysleu         96           c-Myb         Pro⁵²¹ LeuLeuLysLyslieLysGin         98           p53         Pro³¹¹6GlnProLysLysLysleySro         99           Nucleolin         Pro²²¹² GlyLysArgLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly⁴8ArgLysLysArgArgGlnArgArgArgArgArgArgArgArgArgArgArgArgArgA	SOURCE	SEQUENCE	SEQ ID NO.
Human c-Myc         Pro¹²² AlaAlaLysArgValLysLeuAsp         92           Adenovirus E1A         Lys²²²² ArgProArgPro         93           Yeast mat α2         Lys³¹leProIleLys         94           A. Gly²²LysArgLysArgLysSer         95           c-Erb-A         B. Ser¹²²LysArgValAlaLysArgLysleu         96           C. Ser¹³¹HisTrpLysGlnLysArgLysPhe         97           c-Myb         Pro⁵²¹LeuLeuLysLysIleLysGln         98           p53         Pro³¹¹6GlnProLysLysLysPro         99           Nucleolin         Pro²²²¬GlyLysArgLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly⁴³ArgLysLysArgArgGlnArgArgArgArgArgArgArgArgArgArgArgArgArgA	SV40 large T	Pro 126 Lys Lys Arg Lys Val Glu	90
Adenovirus E1A         Lys²8¹ ArgProArgPro         93           Yeast mat α2         Lys³ IleProIleLys         94           c-Erb-A         B. Ser¹²² LysArgLysArgLysSer         95           c-Erb-A         B. Ser¹²² LysArgValAlaLysArgLysleu         96           C. Ser¹¹¹ HisTrpLysGlnLysArgLysPhe         97           c-Myb         Pro⁵²¹ LeuLeuLysLysIleLysGln         98           p53         Pro³¹¹ GlnProLysLysLysPro         99           Nucleolin         Pro²²¹ GlyLysArgLysLysGluMetThrLysGinLysGluValPro         100           HIV Tat         Gly⁴² ArgLysLysArgArgGlnArgArgArgArgAlaPro         101           FGF-1         AsnTyrLysLysProLysLeu         102           FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF 189         LysArgLysArgLysLys (in EXON VI)         85           VEGF 206         LysArgLysArgLysLys (in EXON VI)         85	Polyoma large T	Pro <sup>279</sup> ProLysLysAlaArgGluVal	91
Yeast mat α2         Lys³IleProlleLys         94           c-Erb-A         B. Ser¹²²LysArgLysArgLysArgLysleu         96           C. Ser¹8¹HisTrpLysGlnLysArgLysPhe         97           c-Myb         Pro⁵²¹LeuLeuLysLysIleLysGln         98           p53         Pro³¹¹6GlnProLysLysLysPro         99           Nucleolin         Pro²²'7GlyLysArgLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly⁴8ArgLysLysArgArgGinArgArgArgArgAlaPro         101           FGF-1         AsnTyrLysLysProLysLeu         102           FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF 189         LysArgLysArgLysLys (in EXON VI)         85           VEGF 206         LysArgLysArgLysLys (in EXON VI)         85	Human c-Myc	Pro 120 Ala Ala Lys Arg Val Lys Leu Asp	92
c-Erb-A         A. Gly <sup>22</sup> LysArgLysArgLysSer         95           B. Ser <sup>127</sup> LysArgValAlaLysArgLysleu         96           C. Ser <sup>181</sup> HisTrpLysGlnLysArgLysPhe         97           c-Myb         Pro <sup>521</sup> LeuLeuLysLysIleLysGin         98           p53         Pro <sup>316</sup> GlnProLysLysLysIleLysGin         99           Nucleolin         Pro <sup>277</sup> GlyLysArgLysLysGluMetThrLysGlnLysGluValPro         100           HIV Tat         Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgArgArgAlaPro         101           FGF-1         AsnTyrLysLysProLysLeu         102           FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	Adenovirus E1A	Lys <sup>281</sup> ArgProArgPro	93
c-Erb-A  B. Ser <sup>127</sup> LysArgValAlaLysArgLysleu  C. Ser <sup>181</sup> HisTrpLysGlnLysArgLysPhe  97  c-Myb  Pro <sup>521</sup> LeuLeuLysLysIleLysGln  98  p53  Pro <sup>316</sup> GlnProLysLysLysPro  99  Nucleolin  Pro <sup>277</sup> GlyLysArgLysLysGluMetThrLysGlnLysGluValPro  HIV Tat  Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgArgAlaPro  101  FGF-1  AsnTyrLysLysProLysLeu  102  FGF-2  HisPheLysAspProLysArg  103  FGF-3  AlaProArgArgArgLysLeu  72  FGF-4  IleLysArgLeuArgArg  75  FGF-5  GlyArgArg  FGF-6  IleLysArgGlnArgArg  76  FGF-7  IleArgValArgArg  84  VEGF189  LysArgLysArgLysLys (in EXON VI)  85  VEGF206  LysArgLysArgLysLys (in EXON VI)  85	Yeast mat α2	Lys <sup>3</sup> IleProIleLys	94
C. Ser <sup>181</sup> HisTrpLysGinLysArgLysPhe 97  c-Myb Pro <sup>521</sup> LeuLeuLysLysIleLysGin 98  p53 Pro <sup>316</sup> GlnProLysLysLysPro 99  Nucleolin Pro <sup>277</sup> GlyLysArgLysLysGluMetThrLysGinLysGiuValPro 100  HIV Tat Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgAlaPro 101  FGF-1 AsnTyrLysLysProLysLeu 102  FGF-2 HisPheLysAspProLysArg 103  FGF-3 AlaProArgArgArgLysLeu 72  FGF-4 IleLysArgLeuArgArg 75  FGF-5 GlyArgArg 76  FGF-6 IleLysArgGinArgArg 76  FGF-7 IleArgValArgArg 84  VEGF189 LysArgLysArgLysLys (in EXON VI) 85  VEGF206 LysArgLysArgLysLys (in EXON VI)			95
c-Myb Pro <sup>521</sup> LeuLeuLysLysIleLysGin 98 p53 Pro <sup>316</sup> GlnProLysLysLysPro 99 Nucleolin Pro <sup>277</sup> GlyLysArgLysLysGluMetThrLysGlnLysGluValPro 100 HIV Tat Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgAlaPro 101 FGF-1 AsnTyrLysLysProLysLeu 102 FGF-2 HisPheLysAspProLysArg 103 FGF-3 AlaProArgArgArgLysLeu 72 FGF-4 IleLysArgLeuArgArg 75 FGF-5 GlyArgArg - FGF-6 IleLysArgGlnArgArg 76 FGF-7 IleArgValArgArg 84 VEGF189 LysArgLysArgLysLys (in EXON VI) 85 VEGF206 LysArgLysArgLysLys (in EXON VI) 85	c-Erb-A	B. Ser 127 Lys Arg Val Ala Lys Arg Lysleu	96
Pro <sup>316</sup> GlnProLysLysLysPro  Nucleolin Pro <sup>277</sup> GlyLysArgLysLysGluMetThrLysGlnLysGluValPro  HIV Tat Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgArgAlaPro  101  FGF-1 AsnTyrLysLysProLysLeu  102  FGF-2 HisPheLysAspProLysArg  103  FGF-3 AlaProArgArgArgLysLeu  72  FGF-4 IleLysArgLeuArgArg  FGF-5 GlyArgArg  FGF-6 IleLysArgGlnArgArg  FGF-7 IleArgValArgArg  VEGF189 LysArgLysArgLysLys (in EXON VI)  85  VEGF206 LysArgLysArgLysLys (in EXON VI)  85		C. Ser <sup>181</sup> HisTrpLysGlnLysArgLysPhe	97
NucleolinPro277GlyLysArgLysLysGluMetThrLysGlnLysGluValPro100HIV TatGly48ArgLysLysArgArgGlnArgArgArgArgAlaPro101FGF-1AsnTyrLysLysProLysLeu102FGF-2HisPheLysAspProLysArg103FGF-3AlaProArgArgArgLysLeu72FGF-4IleLysArgLeuArgArg75FGF-5GlyArgArg-FGF-6IleLysArgGlnArgArg76FGF-7IleArgValArgArg84VEGF189LysArgLysArgLysLys (in EXON VI)85VEGF206LysArgLysArgLysLys (in EXON VI)85	c-Myb	Pro <sup>521</sup> LeuLeuLysLysIleLysGin	98
HIV Tat Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgAlaPro 101  FGF-1 AsnTyrLysLysProLysLeu 102  FGF-2 HisPheLysAspProLysArg 103  FGF-3 AlaProArgArgArgLysLeu 72  FGF-4 IleLysArgLeuArgArg 75  FGF-5 GlyArgArg -  FGF-6 IleLysArgGlnArgArg 76  FGF-7 IleArgValArgArg 84  VEGF189 LysArgLysArgLysLys (in EXON VI) 85  VEGF206 LysArgLysArgLysLys (in EXON VI) 85	p53	Pro <sup>316</sup> GlnProLysLysPro	99
FGF-1         AsnTyrLysLysProLysLeu         102           FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	Nucleolin	$Pro^{277}GlyLysArgLysLysGluMetThrLysGlnLysGluValPro\\$	100
FGF-2         HisPheLysAspProLysArg         103           FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	HIV Tat	Gly <sup>48</sup> ArgLysLysArgArgGlnArgArgArgAlaPro	101
FGF-3         AlaProArgArgArgLysLeu         72           FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	FGF-1	AsnTyrLysLysProLysLeu	102
FGF-4         IleLysArgLeuArgArg         75           FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	FGF-2	HisPheLysAspProLysArg	103
FGF-5         GlyArgArg         -           FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	FGF-3	AlaProArgArgArgLysLeu	72
FGF-6         IleLysArgGlnArgArg         76           FGF-7         IleArgValArgArg         84           VEGF189         LysArgLysArgLysLys (in EXON VI)         85           VEGF206         LysArgLysArgLysLys (in EXON VI)         85	FGF-4	IleLysArgLeuArgArg	75
FGF-7 IleArgValArgArg 84  VEGF189 LysArgLysArgLysLys (in EXON VI) 85  VEGF206 LysArgLysArgLysLys (in EXON VI) 85	FGF-5	GlyArgArg	-
VEGF189LysArgLysArgLysLys (in EXON VI)85VEGF206LysArgLysArgLysLys (in EXON VI)85	FGF-6	IleLysArgGlnArgArg	76
VEGF206 LysArgLysArgLysLys (in EXON VI) 85	FGF-7	IleArgValArgArg	84
	VEGF189	LysArgLysArgLysLys (in EXON VI)	85
PDGF ProLysGlyLysHisArgLysPheLysHisThr	VEGF <sub>206</sub>	LysArgLysArgLysLys (in EXON VI)	85
	PDGF	ProLysGlyLysHisArgLysPheLysHisThr	

<sup>\*</sup>Superscript indicates position in protein

### 2. Cytoplasm-translocation signal

Cytoplasm-translocation signal sequence is a sequence of amino acids in a protein that cause retention of proteins in the lumen of the endoplasmic reticulum and/or translocate proteins to the cytosol. The signal sequence in mammalian cells is KDEL (Lys-Asp-Glu-Leu) (Munro and Pelham, Cell 48:899-907, 1987). Some modifications of this sequence have been made without loss of activity. For example, the sequences RDEL (Arg-Asp-Glu-Leu) and KEEL (Lys-Glu-Glu-Leu) confer efficient or partial retention, respectively, in plants (Denecke et al., Embo. J. 11:2345-2355, 1992).

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A cytoplasm-translocation signal sequence may be included in saporin or, for conjugates of VEGF with a nucleic acid binding domain, the sequence may reside in either part or both. If cleavable linkers are used in the conjugate, the cytoplasm-translocation signal is preferably included in saporin or the nucleic acid binding domain. Additionally, a cytoplasmic-translocation signal sequence may be included in VEGF, as long as it is placed so as not to interfere with receptor binding.

In addition, or alternatively, membrane-disruptive peptides may be incorporated into complexes of VEGF-nucleic acid binding domain and cytocide-encoding agent. Adenoviruses are known to enhance disruption of endosomes. Virus-free viral proteins, such as influenza virus hemagglutinin HA-2, may be useful in the present invention. Other proteins may be tested in the assays described herein to find specific endosome disrupting agents that enhance gene delivery. In general, these proteins and peptides are amphipathic (see, Wagner et al., Adv. Drug. Del. Rev. 14:113-135, 1994).

### 15 3. Linkers

A linker is a peptide or other molecule that couples a VEGF polypeptide to the targeted agent. The linker may be bound via the N- or C-terminus or an internal reside, but, typically within about 20 amino acids of either terminus of a VEGF and/or targeted agent. The linkers provided herein increase intracellular availability, serum stability, specificity and solubility of the conjugate or provide increased flexibility or relieve steric hindrance in the conjugate. For example, specificity or intracellular availability of the targeted agent of may be conferred by including a linker that is a substrate for certain proteases, such as a protease that is present in only certain subcellular compartments or that are present at higher levels in tumor cells than normal cells.

In order to increase the serum stability, solubility and/or intracellular concentration and to reduce steric hindrance caused by close proximity of VEGF and the targeted agent, one or more linkers is (are) inserted between the VEGF protein and the targeted moiety. These linkers include peptide linkers, such as intracellular protease substrates and peptides that increase flexibility or solubility of the linked moieties, and chemical linkers, such as acid labile linkers, ribozyme substrate linkers and others. Peptide linkers may be inserted using heterobiofunctional reagents, described below, or, preferably, are linked to VEGF by linking DNA encoding the substrate to the DNA encoding the VEGF protein and expressing the resulting chimera. In instances in which the targeted agent is a protein, such as a RIP, the DNA encoding the linker can be inserted between the DNA encoding the VEGF protein and the DNA encoding the targeted protein agent.

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Chemical linkers may be inserted by covalently coupling the linker to the VEGF protein and the targeted agent. The heterobifunctional agents, described below, may be used to effect such covalent coupling.

#### a. Protease substrates

Peptides encoding protease-specific substrates are introduced between the VEGF protein and the targeted moiety. The peptides may be inserted using heterobiofunctional reagents, described below, or, preferably, are linked to VEGF by linking DNA encoding the substrate to the DNA encoding the VEGF protein and expressing the resulting chimera. In instances in which the targeted agent is a protein, such as a RIP, the DNA encoding the linker can be inserted between the DNA encoding the VEGF protein and the DNA encoding the targeted protein agent. For example, DNA encoding substrates specific for intracellular proteases has been inserted between the DNA encoding the VEGF protein and a targeted agent, such as saporin.

Any protease specific substrate (see, e.g., O'Hare et al. (1990) FEBS 273:200-204; Forsberg et al. (1991) J. Protein Chem. 10:517-526; Westby et al. (1992) Bioconjuugate Chem. 3:375-381) may be introduced as a linker between the VEGF polypeptide and linked targeting agent as long as the substrate is cleaved in an intracellular compartment. Preferred substrates include those that are specific for proteases that are expressed at higher levels in tumor cells or that are preferentially expressed in the endosome. The following substrates are among those contemplated for use in accord with the methods herein: cathepsin B substrate, cathepsin D substrate, trypsin substrate, thrombin substrate, and recombinant subtilisin substrate (XaaAspGluLeu SEQ ID NO. 50, particularly, PheAlaHisTyr, SEQ ID NO. 49).

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# b. Flexible linkers and linkers that increase the solubility of the conjugates

SEQ ID NO. 42

Flexible linkers and linkers that increase solubility of the conjugates are contemplated for use, either alone or with other linkers, such as the protease specific substrate linkers. Such linkers include, but are not limited to,  $(Gly4Ser)_n$ ,  $(Ser4Gly)_n$  and  $(AlaAlaProAla)_n$  (see, SEQ ID NO. 48) in which n is 1 to 6, preferably 1-4, such as:

(1) Gly4Ser SEQ ID NO. 40 CCATGGGCGG CGGCGGCTCT GCCATGG

(3)

(2) (Gly4Ser)2 SEQ ID NO. 41 CCATGGGCGG CGGCGGCTCT GGCGGCGGCG GCTCTGCCAT GG

(Ser4Gly)4

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CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCGC CATGG

(4) (Ser4Gly)<sub>2</sub> SEQ ID NO. 43

CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCGC CATGG

(5) (AlaAlaProAla)<sub>n</sub>, where n is 1 to 4,

preferably 2 (see, SEQ ID NO.:48)

The linker Gly4Ser (SEQ ID No. 40) is preferred for VEGF-VEGF conjugates. The linker Ala-Met is preferred for SAP-VEGF chemical conjugates, and no linker is preferred for SAP-VEGF fusion proteins. In general, a linker length of 1 is preferred for conferring stability on the conjugates.

## c. Heterobifunctional cross-linking reagents

Numerous heterobifunctional cross-linking reagents that are used to form covalent bonds between amino groups and thiol groups and to introduce thiol 15 groups into proteins, are known to those of skill in this art (see. e.g., the Pierce Catalog, ImmunoTechnology Catalog & Handbook, 1992-1993, which describes the preparation of and use of such reagents and provides a commercial source for such reagents; see, also, e.g., Cumber et al. (1992) Bioconjugate Chem. 3:397-401; Thorpe et al. (1987) Cancer Res. 47:5924-5931; Gordon et al. (1987) Proc. Natl. Acad Sci. 84:308-312; 20 Walden et al. (1986) J. Mol. Cell Immunol. 2:191-197; Carlsson et al. (1978) Biochem. J. 173: 723-737; Mahan et al. 91987) Anal. Biochem. 162:163-170; Wawryznaczak et al. (1992) Br. J. Cancer 66:361-366; Fattom et al. (1992) Infection & Immun. 60:584-These reagents may be used to form covalent bonds between the VEGF 589). polypeptide(s) with protease substrate peptide linkers and targeted protein agent. These 25 reagents include, but are not limited to: N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP; disulfide linker); sulfosuccinimidyl 6-[3-(2-pyridyldithio)propionamido]hexanoate (sulfo-LC-SPDP); succinimidyloxycarbonyl-\alpha-methyl thiosulfate (SMBT, hindered disulfate linker); succinimidyl 6-[3-(2-pyridyldithio) 30 propionamido]hexanoate (LC-SPDP); sulfosuccinimidyl 4-(Nmaleimidomethyl)cyclohexane-1-carboxylate (sulfo-SMCC): succinimidyl 3-(2pyridyldithio)butyrate (SPDB; hindered disulfide bond linker); sulfosuccinimidyl 2-(7azido-4-methylcoumarin-3-acetamide) ethyl-1.3'-dithiopropionate (SAED); sulfosuccinimidyl 7-azido-4-methylcoumarin-3-acetate (SAMCA): sulfosuccinimidyl 6-[alpha-methyl-alpha-(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-SMPT); 1.4-di-35 [3'-(2'-pyridyldithio)propionamido]butane (DPDPB); 4-succinimidyloxycarbonyl- $\alpha$ methyl-\alpha-(2-pyridylthio)toluene (SMPT, hindered disulfate linker):sulfosuccinimidyl6[

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α-methyl-α-(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-SMPT); maleimidobenzoyl-N-hydroxysuccinimide ester (MBS); m-maleimidobenzoyl-Nhydroxysulfosuccinimide ester (sulfo-MBS); N-succinimidyl(4iodoacetyl)aminobenzoate (SIAB: thioether linker); sulfosuccinimidyl(4iodoacetyl)amino benzoate (sulfo-SIAB); succinimidyl4(p-maleimidophenyl)butyrate (SMPB); sulfosuccinimidyl4-(p-maleimidophenyl)butyrate (sulfo-SMPB); azidobenzoyl hydrazide (ABH). These linkers should be particularly useful when used in combination with peptide linkers, such as those that increase flexibility.

## d. Acid cleavable, photocleavable and heat sensitive linkers

Acid cleavable linkers include, but are not limited to, bismaleimideothoxy propane; and adipic acid dihydrazide linkers (see, e.g., Fattom et al. (1992) Infection & Immun. 60:584-589) and acid labile transferrin conjugates that contain a sufficient portion of transferrin to permit entry into the intracellular transferrin cycling pathway (see, e.g., Welhöner et al. (1991) J. Biol. Chem. 266:4309-4314). Conjugates linked via acid cleavable linkers should be preferentially cleaved in acidic intracellular compartments, such as the endosome.

Photocleavable linkers are linkers that are cleaved upon exposure to light (see, e.g., Goldmacher et al. (1992) Bioconj. Chem. 3:104-107, which linkers are herein incorporated by reference), thereby releasing the targeted agent upon exposure to light. Photocleavable linkers are linkers that are cleaved upon exposure to light are known (see, e.g., Hazum et al. (1981) in Pept., Proc. Eur. Pept. Symp., 16th, Brunfeldt, K (Ed), pp. 105-110, which describes the use of a nitrobenzyl group as a photocleavable protective group for cysteine; Yen et al. (1989) Makromol. Chem. 190:69-82, which describes water soluble photocleavable copolymers. including hydroxypropylmethacrylamide copolymer, glycine copolymer, fluorescein copolymer and methylrhodamine copolymer; Goldmacher et al. (1992) Bioconj. Chem. 3:104-107. which describes a cross-linker and reagent therefor that undergoes photolytic degradation upon exposure to near UV light (350 nm); and Senter et al. (1985) Photochem. Photobiol 42:231-237, which describes nitrobenzyloxycarbonyl chloride cross linking reagents that produce photocleavable linkages), thereby releasing the targeted agent upon exposure to light. Such linkers would have particular use in treating dermatological or ophthalmic conditions that can be exposed to light using fiber optics. After administration of the conjugate, the eye or skin or other body part can be exposed to light, resulting in release of the targeted moiety from the conjugate. If the toxic moiety is a light activated porphyrin, light-exposure will also activate the porphyrin, thereby causing cell death. Use of photocleavable linkers should permit

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administration of higher dosages of such conjugates compared to conjugates that release a cytotoxic agent upon internalization. Heat sensitive linkers would also have similar applicability.

# 5 D. Expression vectors and host cells for expression of VEGF or targeted agents.

DNA encoding the desired VEGF, polypeptide targeted agent or VEGF conjugate is inserted into a suitable vector and expressed in a suitable prokaryotic or eukaryotic host. Numerous suitable hosts and vectors are known and available to those of skill in this art and may be purchased commercially or constructed according to published protocols using well known and available starting materials. Suitable eukaryotic host cells include insect cells, yeast cells, and animal cells. Suitable prokaryotic host cells include *E. coli*, strains of *Bacillus* and *Streptomyces*. *E. coli* is a preferred host cell.

The DNA construct is introduced into a plasmid for expression in a desired host. In preferred embodiments, the host is a bacterial host. The sequences of nucleotides in the plasmids that are regulatory regions, such as promoters and operators, are operationally associated with one another for transcription. The sequence of nucleotides encoding the growth factor or growth factor-chimera may also include DNA encoding a secretion signal, whereby the resulting peptide is a precursor protein. The resulting processed protein may be recovered from the periplasmic space or the fermentation medium.

In preferred embodiments the DNA plasmids also include a transcription terminator sequence. The promoter regions and transcription terminators are each independently selected from the same or different genes.

The plasmids used herein include a promoter in operable association with the DNA encoding the protein or polypeptide of interest and are designed for expression of proteins in a bacterial host. It has been found that tightly regulated promoters are preferred for expression of saporin. Suitable promoters for expression of proteins and polypeptides herein are widely available and are well known in the art. Inducible promoters or constitutive promoters that are linked to regulatory regions are preferred. Examples of suitable inducible promoters and promoter regions include, but are not limited to: the *E. coli* lac operator responsive to isopropyl β-D-thiogalactopyranoside (IPTG; see, et al. Nakamura et al. (1979) *Cell 18*:1109-1117); the metallothionein promoter metal-regulatory-elements responsive to heavy-metal (e.g., zinc) induction (see, e.g., U.S. Patent No. 4,870,009 to Evans et al.); the

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phage T7lac promoter responsive to IPTG (see, e.g., U.S. Patent No. 4,952,496; and Studier et al. (1990) Meth. Enzymol. 185:60-89) and the tac promoter. Other promoters include, but are not limited to, the T7 phage promoter and other T7-like phage promoters, such as the T3, T5 and SP6 promoters, the trp, lpp, and lac promoters, such as the lacUV5, from E. coli; the P10 or polyhedron gene promoter of baculovirus/insect cell expression systems (see, e.g., U.S. Patent Nos. 5.243,041, 5,242,687, 5,266,317, 4,745,051, and 5,169,784) and inducible promoters from other eukaryotic expression systems.

Preferred promoter regions are those that are inducible and functional in *E. coli*. Examples of suitable inducible promoters and promoter regions include, but are not limited to: the *E. coli* lac operator responsive to isopropyl β-D-thiogalactopyranoside (IPTG; see, et al. Nakamura et al., Cell 18:1109-1117, 1979); the metallothionein promoter metal-regulatory-elements responsive to heavy-metal (e.g., zinc) induction (see, e.g., U.S. Patent No. 4,870,009 to Evans et al.); the phage T7lac promoter responsive to IPTG (see, e.g., U.S. Patent No. 4,952,496; and Studier et al., Meth. Enzymol. 185:60-89, 1990) and the tac promoter.

The plasmids also preferably include a selectable marker gene or genes that are functional in the host. A selectable marker gene includes any gene that confers a phenotype on bacteria that allows transformed bacterial cells to be identified and selectively grown from among a vast majority of untransformed cells. Suitable selectable marker genes for bacterial hosts, for example, include the ampicillin resistance gene (Amp<sup>r</sup>), tetracycline resistance gene (Tc<sup>r</sup>) and the kanamycin resistance gene (Kan<sup>r</sup>). The kanamycin resistance gene is presently preferred.

The plasmids may also include DNA encoding a signal for secretion of 25 the operably linked protein. Secretion signals suitable for use are widely available and are well known in the art. Prokaryotic and eukaryotic secretion signals functional in E. coli may be employed. The presently preferred secretion signals include, but are not limited to, those encoded by the following E. coli genes: ompA, ompT, ompF, ompC. beta-lactamase, and alkaline phosphatase, and the like (von Heijne, J. Mol. Biol. 30 184:99-105, 1985). In addition, the bacterial pelB gene secretion signal (Lei et al., J. Bacteriol. 169:4379, 1987), the phoA secretion signal, and the cek2 functional in insect cell may be employed. The most preferred secretion signal is the E. coli ompA secretion signal. Other prokaryotic and eukaryotic secretion signals known to those of skill in the art may also be employed (see, e.g., von Heijne, J. Mol. Biol. 184:99-105. 1985). Using the methods described herein, one of skill in the art can substitute 35 secretion signals that are functional in either yeast, insect or mammalian cells to secrete proteins from those cells.

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Preferred plasmids for transformation of *E. coli* cells include the pET expression vectors (*see*, U.S patent 4,952,496; available from Novagen, Madison, WI; *see*, *also*, literature published by Novagen describing the system). Such plasmids include pET 11a, which contains the T7lac promoter, T7 terminator, the inducible *E. coli* lac operator, and the lac repressor gene; pET 12a-c, which contains the T7 promoter, T7 terminator, and the *E. coli* ompT secretion signal; and pET 15b (Novagen, Madison, WI), which contains a His-Tag<sup>TM</sup> leader sequence (Seq. ID No. 36) for use in purification with a His column and a thrombin cleavage site that permits cleavage following purification over the column; the T7-lac promoter region and the T7 terminator.

Other preferred plasmids include the pKK plasmids, particularly pKK 223-3, which contains the tac promoter, (available from Pharmacia; see, also, Brosius et al., Proc. Natl. Acad. Sci. 81:6929, 1984; Ausubel et al., Current Protocols in Molecular Biology; U.S. Patent Nos. 5,122,463, 5,173,403, 5,187,153, 5,204,254, 5,212,058, 5,212,286, 5,215,907, 5,220,013, 5,223,483, and 5,229,279). Plasmid pKK has been modified by replacement of the ampicillin resistance marker gene, by digestion with EcoRI, with a kanamycin resistance cassette with EcoRI sticky ends (purchased from Pharmacia; obtained from pUC4K, see, e.g., Vieira et al. (Gene 19:259-268, 1982; and U.S. Patent No. 4,719,179) into the ampicillin resistance marker gene.

Baculovirus vectors, such as a pBlueBac (also called pJVETL and derivatives thereof) vector, particularly pBlueBac III, (see, e.g., U.S. Patent Nos. 5,278,050, 5,244,805, 5,243,041, 5,242,687, 5,266,317, 4,745.051, and 5,169,784; available from Invitrogen, San Diego) may also be used for expression of the polypeptides in insect cells. The pBlueBacIII vector is a dual promoter vector and provides for the selection of recombinants by blue/white screening as this plasmid contains the β-galactosidase gene (lacZ) under the control of the insect recognizable ETL promoter and is inducible with IPTG. A DNA construct may be made in baculovirus vector pBluebac III (Invitrogen, San Diego, CA) and then co-transfected with wild type virus into insect Spodoptera frugiperda cells (sf9 cells: see, e.g., Luckow et al., Bio/technology 6:47-55, 1988, and U.S. Patent No. 4,745,051).

Other plasmids include the pIN-IIIompA plasmids (see, U.S. Patent No. 4.575,013 to Inouye; see, also, Duffaud et al., Meth. Enz. 153:492-507, 1987), such as pIN-IIIompA2. The pIN-IIIompA plasmids include an insertion site for heterologous DNA linked in transcriptional reading frame with four functional fragments derived from the lipoprotein gene of E. coli. The plasmids also include a DNA fragment coding for the signal peptide of the ompA protein of E. coli, positioned such that the desired

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polypeptide is expressed with the ompA signal peptide at its amino terminus, thereby allowing efficient secretion across the cytoplasmic membrane. The plasmids further include DNA encoding a specific segment of the *E. coli* lac promoter-operator, which is positioned in the proper orientation for transcriptional expression of the desired polypeptide, as well as a separate functional *E. coli* lacI gene encoding the associated repressor molecule that, in the absence of lac operon inducer, interacts with the lac promoter-operator to prevent transcription therefrom. Expression of the desired polypeptide is under the control of the lipoprotein (lpp) promoter and the lac promoter-operator, although transcription from either promoter is normally blocked by the repressor molecule. The repressor is selectively inactivated by means of an inducer molecule thereby inducing transcriptional expression of the desired polypeptide from both promoters.

A particularly preferred vector for expressing VEGF protein is  $pP_L-\lambda$  (Pharmacia Biotech, Uppsala, Sweden). This vector contains the tightly regulated leftward promoter of bacteriophage  $\lambda$ , which is controlled by the cl repressor. The promoter is temperature-inducible by using a bacterial host strain, such as N4830-1, containing the temperature-sensitive cl857 repressor. The vector contains a unique *Hpal* site for cloning. *Hpal* digestion leaves blunt ends. The VEGF on VEGF-cytotoxic agent, such as VEGF-SAP, is prepared as a blunt-end fragment (see Examples) and ligated into  $pP_L-\lambda$ . Inclusion bodies containing the protein are isolated, solubilized and refolded.

Preferably, the DNA fragment is replicated in bacterial cells, preferably in *E. coli*. The preferred DNA fragment also includes a bacterial origin of replication, to ensure the maintenance of the DNA fragment from generation to generation of the bacteria. In this way, large quantities of the DNA fragment can be produced by replication in bacteria. Preferred bacterial origins of replication include, but are not limited to, the f1-ori and colE1 origins of replication. Preferred hosts contain chromosomal copies of DNA encoding T7 RNA polymerase operably linked to an inducible promoter, such as the lacUV promoter (see, U.S. Patent No. 4,952,496). Such hosts include, but are not limited to, lysogenic *E. coli* strains HMS174(DE3)pLysS, BL21(DE3)pLysS, HMS174(DE3) and BL21(DE3). Strain BL21(DE3) is preferred. The pLys strains provide low levels of T7 lysozyme, a natural inhibitor of T7 RNA polymerase.

The DNA fragments provided may also contain a gene coding for a repressor-protein. The repressor-protein is capable of repressing the transcription of a promoter that contains sequences of nucleotides to which the repressor-protein binds. The promoter can be derepressed by altering the physiological conditions of the cell.

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The alteration can be accomplished by the addition to the growth medium of a molecule that inhibits, for example, the ability to interact with the operator or with regulatory proteins or other regions of the DNA or by altering the temperature of the growth media. Preferred repressor-proteins include, but are not limited to the *E. coli.* lacI repressor responsive to IPTG induction, the temperature sensitive cl857 repressor, and the like. The cl857 repressor is particularly preferred.

The DNA construct is introduced into a plasmid suitable for expression in the selected host. The sequences of nucleotides in the plasmids that are regulatory regions, such as promoters and operators, are operationally associated with one another for transcription. The sequence of nucleotides encoding the VEGF, VEGF chimera or cytotoxic agent may also include DNA encoding a secretion signal, whereby the resulting peptide is a precursor protein. Secretion signals suitable for use are widely available and are well known in the art. Prokaryotic and eukaryotic secretion signals functional in E. coli, may be employed. The presently preferred secretion signals include, but are not limited to, those encoded by the following E. coli genes: ompA, ompT, ompF, ompC, beta-lactamase, pelB and bacterial alkaline phosphatase, and the like (von Heijne (1985) J. Mol. Biol. 184:99-105). In addition, the bacterial pelB gene secretion signal (Lei et al. (1987) J. Bacteriol. 169:4379, 1987), the phoA secretion signal, and the cek2 secretion signal, functional in insect cells, may be employed. The most preferred secretion signal for bacterial expression is the E. coli ompA secretion signal. For eukaryotic expression systems, particularly insect cell systems, the signals from secreted proteins, such as insulin, growth hormone, mellitin, and mammalian alkaline phosphatase are of interest herein. Other prokaryotic and eukaryotic secretion signals known to those of skill in the art may also be employed (see. e.g., von Heijne (1985) J. Mol. Biol. 184:99-105). Using the methods described herein, one of skill in the art can substitute secretion signals that are functional in either yeast, insect or mammalian cells to secretes the heterologous protein from those cells. The resulting processed protein may be recovered from the periplasmic space or the fermentation medium or growth medium.

In certain preferred embodiments, the constructs also include a transcription terminator sequence. The promoter regions and transcription terminators are each independently selected from the same or different genes. In some embodiments, the DNA fragment is replicated in bacterial cells, preferably in *E. coli*. The DNA fragment also typically includes a bacterial origin of replication, to ensure the maintenance of the DNA fragment from generation to generation of the bacteria. In this way, large quantities of the DNA fragment can be produced by replication in bacteria.

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Preferred bacterial origins of replication include, but are not limited to, the fl-ori and col E1 origins of replication.

DNA encoding full-length VEGF, VEGF-SAP, SAP-VEGF with and without linkers, and other such constructs, are introduced into the pET vectors, preferably pET-11a (Novagen, Madison, WI) or the pP<sub>L</sub>- $\lambda$  vector (Pharmacia). It is found that for expression in bacterial hosts that constructs in which DNA encoding SAP is linked, directly or via a linker, to DNA encoding the N-terminus of VEGF is preferred. When the SAP-VEGF<sub>121</sub> or SAP-VEGF<sub>165</sub> is produced in pP<sub>L</sub>- $\lambda$ , no linker is preferable. Also, constructs containing DNA encoding two monomers, which upon expression, dimerize, preferably in an antiparallel manner, are preferred.

### E. Method of preparation of VEGF-targeted agent conjugates

Conjugates that contain one or more VEGF polypeptides linked, either directly or via a linker, to one or more targeted agents are provided. The presently preferred VEGF monomers are VEGF165 and VEGF121. VEGF121 is particularly preferred.

As described above, the conjugates contain the following components: (VEGF)<sub>n</sub>, (L)<sub>q</sub>, and (targeted agent)<sub>m</sub> in which: at least one VEGF moiety is linked with or without a linker (L) to at least one targeted agent, n is 1 or more, generally is at least 2, and typically is between 2 and 6; q is 0 or more as long as the resulting conjugate binds to the targeted receptor, is internalized and delivers the targeted agent, q is generally 0 or 1 to 4; m is 1 or more, generally 1 or 2; L refers to a linker, and the targeted agent is any agent, such as a cytotoxic agent or a nucleic acid, or a drug, such as methotrexate, intended for internalization by a cell that expresses a receptor to which VEGF binds and upon binding is internalized. The components may be organized in any order.

It is also understood that substitutions in codons by virtue of the degeneracy of the genetic code are encompassed by DNA encoding such VEGF. DNA encoding the VEGF polypeptide may be obtained from any source known to those of skill in the art; it may be isolated using standard cloning methods, synthesized or obtained from commercial sources, prepared as described in any of the patents and publications noted herein.

In some embodiments, the conjugates provided herein may be represented by the formula (I):

(VEGF<sub>p</sub>-(L)<sub>q</sub>-targeted agent)<sub>n</sub>

in which VEGF refers to a polypeptide that is reactive with a VEGF receptor (also referred to herein as a VEGF protein), such as VEGF. L refers to a

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linker, which may be present or absent, q is 0 or more as long as the resulting conjugate binds to a targeted receptor and the targeted agent is internalized, p is 1 or more. preferably 1, and generally less than or equal to 4, and the targeted agent is any agent. such as a cytotoxic agent or a nucleic acid, or a drug, such as methotrexate, intended for internalization by a cell that expresses a VEGF receptor; n is 1 or 2; and the VEGF may be linked to the linker or targeted agent via its N-terminus or C-terminus or any other locus in polypeptide, such as derivatized cys residues. When n is 2, the conjugates are linked via cysteine residues on the VEGF, probably via residues that correspond to the cysteines at positions 77 and 86 in SEQ ID NOs. 25-28. The linked VEGFs may be linked in a parallel fashion or antiparallel fashion. Conjugates of the formula (II): targeted agent-L-(VEGF)<sub>n</sub>), in which n is 1 or 2, are also provided. These conjugates are prepared by mixing conjugates of formula I with unconjugated VEGF, by preparing fusion proteins from DNA constructs that encode two VEGF moieties, or by mixing conjugates of formulas I and II. The VEGF moieties are preferably linked via a linker to facilitate dimerization.

It is understood that the VEGF and targeted agent (or linker and targeted agent) may be linked in any order and through any appropriate linkage, as long as the resulting conjugate binds to a receptor to which VEGF binds and internalizes the targeted agent(s) in cells bearing the receptor.

For example, the VEGF polypeptide may be linked to the targeted agent or linker at or near its N-terminus or at or near its C-terminus. The VEGF may be linked to a second VEGF monomer, which may be the same monomer or a different monomer; and one or more targeted agents that are the same or different may be linked to the VEGF or may be linked to each other. The linkage may be at any locus, although the N-terminus region of VEGF (within about 20, preferably 10, amino acids from the N-terminus) is preferred. When multiple VEGFs are linked, they may be in a head to head, head to tail or tail to tail orientation. If more than one targeted agent is included, the second may be the same or different from the first agent. In order to efficiently bind to VEGF receptors and deliver a targeted agent to a cell, VEGF dimerization appears to be required.

In addition, conjugates in which non-essential cysteines in the VEGF monomers and/or targeted agent, if the agent is a polypeptide, are deleted or replaced with Ser or other conservative substitution are provided. Compositions of such conjugates should exhibit reduced aggregation compared to conjugates that contain non-essential cysteines. Non-essential cysteines may be identified empirically.

Polypeptides that are reactive with a VEGF receptor (VEGF proteins) include any molecule that reacts with VEGF receptors on cells that bear VEGF

receptors and results in internalization of the linked cytotoxic agent. Particularly preferred polypeptides that are reactive with a VEGF receptor include members of the VEGF family of polypeptides, muteins of these polypeptides, chimeric or hybrid molecules that contain portions of any of these family members, and any portion thereof that binds to VEGF receptors and internalizes a linked agent.

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The linker is selected to increase the specificity, toxicity, solubility, serum stability, and/or intracellular availability targeted moiety. More preferred linkers are those that can be incorporated in fusion proteins and expressed in a host cell, such as *E. coli*. Such linkers include: enzyme substrates, such as cathepsin B substrate, cathepsin D substrate, trypsin substrate, thrombin substrate, subtilisin substrate, factor Xa substrate, and enterokinase substrate; linkers that increase solubility flexibility, and/or intracellular cleavability, such as (glymser)n and (sermgly)n, in which n is 1 to 6, preferably 1 to 4, most preferably 1, and m is 1 to 6, preferably 1 to 4, more preferably 12 to 4, most preferably. Preferred among such linkers, are those, such as cathepsin D substrate, that are preferentially cleaved in the endosome or cytoplasm following internalization of the conjugate linker; other such linkers, such as (glymser)n and (sermgly)n, also increase the flexibility, serum stability and/or solubility of the conjugate or the availability of the region joining the VEGF and targeted agent for cleavage. In some embodiments, several linkers that are the same or different may be included in order to take advantage of desired properties of each linker.

Other linkers are suitable for incorporation into chemically produced conjugates. Linkers that are suitable for chemically linking conjugates include disulfide bonds, thioether bonds, hindered disulfide bonds, and covalent bonds between free reactive groups, such as amine and thiol groups. These bonds are produced using heterobifunctional reagents to produce reactive thiol groups on one or both of the polypeptides and then reacting the thiol groups on one polypeptide with reactive thiol groups or amine groups to which reactive maleimido groups or thiol groups can be attached on the other. Other linkers include acid cleavable linkers, such as bismaleimideothoxy propane, acid labile-transferrin conjugates and adipic acid diihydrazide, that would be cleaved in more acidic intracellular compartments and cross linkers that are cleaved upon exposure to UV or visible light and linkers.

The targeted agents or moieties include any molecule that, when internalized, alter the metabolism or gene expression in the cell. Such agents include cytotoxic agents, such as ribosome inactivating proteins DNA encoding cytotoxic agents, and antisense nucleic acids, that result in inhibition of growth or cell death. Other such agents also include antisense RNA, DNA, and truncated proteins that alter gene expression via interactions with the DNA, or co-suppression or other mechanism.

The conjugates herein may also be used to deliver DNA and thereby serve as agents for gene therapy or to deliver agents that, upon, transcription and/or translation thereof, result in cell death. Cytotoxic agents include, but are not limited to, ribosome inactivating proteins, inhibitors of DNA, RNA and/or protein synthesis, including antisense nucleic acids, and other metabolic inhibitors. In certain embodiments, the cytotoxic agent is a ribosome-inactivating protein (RIP), such as, for example, saporin, although other cytotoxic agents can also be advantageously used.

The targeted agents may also be modified to render them more suitable for conjugation with the linker and/or a VEGF protein or to increase their intracellular activity. Such modifications include, but are not limited to, the introduction of a Cys residue at or near the N-terminus or C-terminus, derivatization to introduce reactive groups, such as thiol groups, and addition of sorting signals, such as (XaaAspGluLeu)n (SEQ ID NO. 50), where Xaa is Lys or Arg, preferably Lys, and n is 1 to 6, preferably 1-3, at, preferably, the carboxy-terminus (see, e.g., Seetharam et al. (1991) J. Biol. Chem. 266:17376-17381; and Buchner et al. (1992) Anal. Biochem. 205:263-270), that direct the targeted agent to the endoplasmic reticulum or the addition of a cytoplasmic sorting sequence, such as KDEL (see discussion herein).

Conjugates that contain a plurality of monomers of a VEGF protein linked to the cytotoxic agent are also provided. These conjugates that contain several, typically two to about six monomers can be produced by linking multiple copies of DNA encoding the VEGF fusion protein, typically head-to-tail, under the transcriptional control of a single promoter region. In addition conjugates that contain, more than one targeted agent per VEGF, such as SAP-VEGF-SAP, linked with or without linkers are contemplated herein.

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### 1. Chemical conjugation

#### a. Preparation of VEGF polypeptides for chemical conjugation

VEGF may be isolated from a suitable source or may be produced using recombinant DNA methodology, discussed below. As used herein, substantially pure means sufficiently homogeneous to appear free of readily detectable impurities as determined by standard methods of analysis, such as thin layer chromatography (TLC), gel electrophoresis, high performance liquid chromatography (HPLC), used by those of skill in the art to assess such purity, or sufficiently pure such that further purification would not detectably alter the physical and chemical properties, such as enzymatic and biological activities, of the substance. Methods for purification of the compounds to produce substantially chemically pure compounds are known to those of skill in the art. A substantially chemically pure compound may, however, be a mixture of

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stereoisomers. In such instances, further purification might increase the specific activity of the compound.

To effect chemical conjugation herein, the VEFG protein is conjugated generally via a reactive amine group or thiol group to the targeted agent or to a linker, which has been or is subsequently linked to the targeted agent. The VEGF protein is conjugated either via its N-terminus, C-terminus, or elsewhere in the polypeptide. In preferred embodiments, the VEGF protein is conjugated via a reactive cysteine residue to the linker or to the targeted agent. The VEGF can also be modified by addition of a cysteine residue, either by replacing a residue or by inserting the cysteine, at or near the amino or carboxyl terminus, within about 20, preferably 10 residues from either end, and preferably at or near the amino terminus.

In preferred embodiments, to reduce the heterogeneity of preparations, the VEGF protein is modified by mutagenesis to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. The VEGF protein is modified by deleting or replacing a site(s) on the VEGF that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of VEGF peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of the VEGF peptide or for retention of the ability to bind to a VEGF receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified VEGF is conjugated with a single species of cytotoxic conjugate.

Alternatively, the contribution of each cysteine to the ability to bind to VEGF receptors may be determined empirically, as described above. Recently the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys 145 in dimerization and biological activity was assessed (Claffery, *supra*). Cys-25, Cys-56, and Cys-67 are required for dimerization; Cys-101 is required for expression. Sustitution of Cys-145 is preferred.

b. Preparation of targeted proteins for chemical conjugation

If the targeted agent is a polypeptide it may be directly linked to the VEGF or VEGF with linker or to a linker by reaction of a reactive group in the polypeptide. It is desirable, however, that the agent may react at only a single locus, so that the resulting preparation of conjugates is homogeneous. Thus, if necessary, the targeted agent can be derivatized and then a single species isolated. Alternatively, and preferably for chemical conjugation, saporin can be modified so that it only has one

reactive group, such as a cysteine, for a particular set of conditions and reagents. For example, saporin has been derivatized and a single species isolated and has also been modified by introduction of a single cysteine residue.

Saporin for chemical conjugation may be produced by isolating the protein from the leaves or seeds of Saponaria officinalis or using recombinant methods and the DNA provided herein or known to those of skill in the art or obtained by screening appropriate libraries (see, e.g., International PCT Application WO 93/25688, which describes the isolation of saporin, plasmids containing DNA encoding saporin. expression of saporin and isolation of purified saporin). Some DNA encoding saporin may also include an N-terminal extension sequence linked to the amino terminus of the saporin that encodes a linker so that, if desired, the SAP and linker can be expressed as a fusion protein as described herein. The sequence of DNA encoding saporin is set forth in SEQ ID Nos. 3-7.

The DNA molecules provided herein encode saporin that has substantially the same amino acid sequence and ribosome-inactivating activity as that 15 of saporin-6 (SO-6), including any of four isoforms, which have heterogeneity at amino acid positions 48 and 91 (see, e.g., Maras et al. (1990) Biochem. Internat. 21:631-638 and Barra et al. (1991) Biotechnol. Appl. Biochem. 13:48-53 and SEQ ID NOs. 3-7). Other suitable saporin polypeptides include other members of the multi-gene family coding for isoforms of saporin-type RIPs including SO-1 and SO-3 (Fordham-Skelton 20 et al. (1990) Mol. Gen. Genet. 221:134-138), SO-2 (see, e.g., U.S. Application Serial No. 07/885,242, which corresponds to GB 2,216,891; see, also, Fordham-Skelton et al. (1991) Mol. Gen. Genet. 229:460-466), SO-4 (see. e.g., GB 2,194,241 B; see, also, Lappi et al. (1985 Biochem. Biophys. Res. Commun. 129:934-942) and SO-5 (see. e.g., GB 2,194,241 B; see, also. Montecucchi et al. (1989) Int. J. Peptide Protein Res., 25 33:263-267; and Ferreras et al. (1993) Biophys. Biochem. Acta 1216:31-42). SO-4. which includes the N-terminal 40 amino acids set forth in SEQ ID NO. 77, is isolated from the leaves of Saponaria officinalis by extraction with 0.1 M phosphate buffer at pH 7, followed by dialysis of the supernatant against sodium borate buffer, pH 9, and 30 selective elution from a negatively charged ion exchange resin, such as Mono S (Pharmacia Fine Chemicals. Sweden) using a gradient of 1 to 0.3 M NaCl and is the first eluting chromatographic fraction that has SAP activity. The second eluting fraction is SO-5.

Because more than one amino group on SAP may react with the succinimidal moiety, it is possible that more than one amino group on the surface of the protein is reactive. This creates the potential for heterogeneity even if monoderivatized SAP is used. This source of heterogeneity has been solved by the

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conjugating modified SAP expressed in *E. coli* that has an additional cysteine inserted in the coding sequence, preferably within 10 or 20 amino acids of either the C-terminus or N-terminus. The preferred molecule has the Met-Cys inserted at the N-terminus.

As discussed above, muteins of saporin that contain a Cys at or near the amino or carboxyl terminus can be prepared. Thus, instead of derivatizing saporin to introduce a sulfhydryl, the saporin can be modified by the introduction of a cysteine residue into the SAP such that the resulting modified saporin protein reacts with a VEGF monomer or a linker (and then to a VEGF monomer) to produce a conjugate. It is understood that, as discussed above and below, in order for the cytotoxic conjugates herein to bind to VEGF receptors most effectively, the VEGF portion of the conjugate should be dimerized.

Preferred loci for introduction of a cysteine residue include the N-terminus region, preferably within about one to twenty residues, more preferably one to about ten residues, from the N-terminus of the cytotoxic agent, such as SAP. For expression of SAP in the bacterial host systems herein, it is also desirable to add DNA encoding a methionine linked to the DNA encoding the N-terminus of the saporin protein. DNA encoding SAP has been modified by inserting a DNA encoding Met-Cys (ATG TGT or ATG TGC) at the N-terminus immediately adjacent to the codon for first residue of the mature protein.

Muteins in which a cysteine residue has been added at the N-terminus and muteins in which the amino acid at position 4 or 10 has been replaced with cysteine have been prepared by modifying the DNA encoding saporin (see, Examples). Preferably, saporin has a cysteine added at the -1 position (see Example 3). The modified DNA may be expressed and the resulting saporin protein purified, as described herein for expression and purification of the resulting SAP. The modified saporin can then be reacted with a VEGF, preferably a VEGF dimer, to form disulfide linkages between the VEGF dimer and the cysteine residue on the modified SAP.

Typically, SAP is derivatized by reaction with SPDP. This results in a heterogeneous population. For example, SAP that is derivatized by SPDP to a level of 0.9 moles pyridine-disulfide per mole of SAP includes a population of non-derivatized. mono-derivatized and di-derivatized SAP. Methods for isolation of mono-derivatized saporin are described, for example, in Lappi et al. (1993) *Anal. Biochem. 212*:446-451, copending U.S. Application Serial No. 08/099,924). The methods rely on the charge differences among the three species of SAP that are produced upon reaction of one ore more lysines in saporin with SPDP. The mono-derivatized saporin species is purified by Mono-S cation exchange chromatography and pooling of the fractions that contain the monoderivatized species. Briefly, the initial eluting peak is composed of SAP that

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is approximately di-derivatized; the second peak is mono-derivatized and the third peak shows no derivatization. The di-derivatized material accounts for 20% of the three peaks; the second accounts for 48% and the third peak contains 32%. Fractions that have a ratio of SPDP to SAP greater than 0.85 but less than 1.05 are pooled, dialyzed against an appropriate buffer, such as 0.1 M sodium chloride, 0.1 M sodium phosphate, pH 7.5, used for coupling to a linker, to a VEGF monomer, a VEGF dimer, a VEGF monomer with linker, or a VEGF dimer with linker.

The resulting preparation, although more uniform, still contains some heterogeneity because native saporin as purified from the seed is a mixture of four isoforms, as judged by protein sequencing (see, e.g., PCT Application WO 93/25688 (Serial No. PCT/US93/05702), United States Application Serial No. 07/901,718; see also, Montecucchi et al. (1989) Int. J. Pept. Prot. Res. 33:263-267; Maras et al. (1990) Biochem. Internat. 21:631-638; and Barra et al. (1991) Biotechnol. Appl. Biochem. 13:48-53). This creates some heterogeneity in the conjugates, since the reaction with SPDP probably occurs equally within each isoform. This source of heterogeneity can be removed by using saporin expressed in E. coli.

# c. Chemical conjugation of a VEGF protein to linkers and targeted agents

The VEGF monomers are preferably linked via non-essential cysteine residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, the VEGF, preferably, is dimerized prior to linkage to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

Methods for chemical conjugation of proteins are known to those of skill in the art. The preferred methods for chemical conjugation depend on the selected components, but preferably rely on disulfide bond formation. For example, if the targeted agent is SPDP-derivatized saporin, then it is advantageous to dimerize the VEGF moiety prior coupling or conjugating to the derivatized saporin.

### 2. Fusion protein of a VEGF polypeptide and targeted agent

Expression of DNA encoding a fusion of a VEGF protein linked to the targeted agent results in a more homogeneous preparation of cytotoxic conjugates and is suitable for use, when the selected targeting agent and linker are polypeptides.

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Aggregate formation may be reduced in preparations containing the fusion proteins by modifying the VEGF, particularly, VEGF165, VEGF189 and VEGF206, which contain nonessential cysteines in the heparin binding domain and/or the targeted agent to prevent cysteine-cysteine interactions between each conjugate or decrease secondary structure.

### a. Expression of VEGF

DNA encoding VEGF peptides and/or the amino acid sequences of VEGFs are known to those of skill in this art (see, e.g., SEQ ID NOs. 18-28). DNA may be prepared synthetically based on the amino acid sequence or known DNA sequence of a VEGF or may be isolated using methods known to those of skill in the art or obtained from commercial or other sources known to those of skill in this art.

It is also understood that substitutions in codons by virtue of the degeneracy of the genetic code are encompassed by DNA encoding such VEGF. DNA encoding the VEGF polypeptide may be obtained from any source known to those of skill in the art; it may be isolated using standard cloning methods, synthesized or obtained from commercial sources, prepared as described in any of the patents and publications noted herein.

Such DNA may then be mutagenized using standard methodologies to delete, replace any cysteine residues, as described herein, that are not required for dimerization and receptor binding and internalization, or insert cysteine residues for chemical conjugation (see, SEQ ID NOs. 86-89). As necessary, the identity of non-essential cysteine residues may be determined empirically, by deleting, inserting and/or and replacing a cysteine residue and ascertaining whether the resulting VEGF with the deleted cysteine form aggregates in solutions containing physiologically acceptable buffers and salts. Loci for insertion of cysteine residues may also be determined empirically. Generally, regions at or near (within 20, preferably 10 amino acids) the C- or, preferably, the N-terminus.

As discussed above, binding to a VEGF receptor followed by internalization are the activities required for a VEGF protein to be suitable for use herein. A test of such activity, which reflects the ability to bind to VEGF receptors and to be internalized, is the ability of a conjugate containing VEGF (e.g., VEGF-saporin) to inhibit proliferation of cells, such as vascular endothelial cells, including bovine or human aortic endothelial cells, that bear VEGF receptors. Any VEGF polypeptide that possesses such ability is intended for use herein.

The DNA encoding the conjugate can be inserted into a plasmid and expressed in a selected host. Multiple copies of the DNA encoding the VEGF-targeted

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agent chimera or VEGF-cytotoxic agent chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will be a VEGF-cytotoxic agent multimer. Typically two to six copies of the chimera are inserted into a plasmid, preferably in a head to tail orientation. Alternatively, one or more copies of the VEGF-targeted agent chimera is inserted under the control of a first promoter in a plasmid and one or more copies encoding a VEGF polypeptide is inserted under the control of a second promoter in the plasmid or into a second plasmid. The resulting plasmid(s) is (are) introduced into a host and cultured under conditions in which the promoter is active and the conjugated and a VEGF polypeptide are produced. The resulting preparation is treated to permit refolding of the VEGF and dimerization. Conjugates containing VEGF dimers are isolated.

# b. Preparation of muteins for recombinant production of the conjugates

15 For recombinant expression using the methods herein, all cysteines in the VEGF peptide that are not required for biological activity can be deleted or replaced; and for use in the chemical conjugation methods herein, all except for one of these cysteines, which will be used for chemical conjugation to the cytotoxic agent, can be deleted or replaced. Human (and the corresponding bovine protein) VEGF121 has nine cysteine residues and VEGF165 and VEGF189 have 16 cysteine residues per monomer. Each of the nine cysteines may be replaced and the resulting mutein tested for the ability to bind to VEGF receptors and to be internalized as described herein. Alternatively, the resulting mutein-encoding DNA is used as part of a construct containing DNA encoding the cytotoxic agent linked to the VEGF-encoding DNA. The construct is expressed in a suitable host cell and the resulting protein tested for the ability to bind to VEGF receptors and internalize the cytotoxic agent. As long this ability is retained the mutein is suitable for use herein.

#### c. DNA constructs and expression of the constructs

DNA encoding VEGF conjugates is expressed in any suitable host. particularly bacterial and insect hosts. Methods and plasmids for such expression are set forth in the examples (see, also Table 3).

Using the methods and materials described above and in the examples numerous chemical conjugates and fusion proteins have been synthesized. These include the constructs set forth in Table 3, below.

Particular details of the syntheses of the constructs are set forth in the EXAMPLES. The constructs have been synthesized and have been or can be inserted

into plasmids including pET 11 (with and without the T7 transcription terminator), pET 12 and pET 15 (Invitrogen, San Diego), pP<sub>1</sub>-λ and pKK223-3 (Pharmacia, P.L.) and derivatives of pKK223-3. The resulting plasmids have been and can be transformed into bacterial hosts including BL21, BL21(DE3), HMS174(DE3), (Novagen, Madison, WI) and N4830(cI857) (see, Gottesman et al. (1980) J. Mol. Biol. 140:57-75, commercially available from PL Biochemicals, Inc., also, see. e.g., U.S. Patent Nos. 5,266,465, 5,260,223, 5,256,769, 5,256,769, 5,252,725, 5,250,296, 5,244,797. 5,236,828, 5,234,829, 5,229,273, 4,798,886, 4,849,350, 4,820,631 and 4,780,313) or N99CI<sup>+</sup> for pP<sub>1</sub>-λ. N4830 harbors a heavily deleted phage lambda prophage carrying the mutant cl857 temperature sensitive repressor and an active N gene. The constructs have also been introduced in baculovirus vector sold commercially under the name pBlueBacIII (Invitrogen, San Diego CA; see the Invitrogen catalog; see, also, Vialard et al. (1990) J. Virol. 64:37; U.S. Patent No. 5,270,458; U.S. Patent No. 5,243,041; and published International PCT Application WO 93/10139, which is based on U.S. patent application Serial No. 07/792,600. The pBlueBacIII vector is a dual promoter vector and provides for the selection of recombinants by blue/white screening as this plasmid contains the \beta-galactosidase gene (lacZ) under the control of the insect recognizable ETL promoter and is inducible with IPTG. The baculovirus vector is then cotransfected with wild type virus into insect host cells Spodoptera frugiperda (sf9; see, e.g., Luckow et al. (1988) Bio/technology 6:47-55 and U.S. Patent No. 4,745,051).

TABLE 3

Plasmid(s)***	Description of Fusion Protein	Fusion Protein Name
PZ50B1	SAP CYS-1	FPS1
PZ51B1	SAP CYS+4	FPS2
PZ51E1	SAP CYS+4	FPS2
PZ52B1	SAP CYS+10	FPS3
PZ52E1	SAP CYS+10	FPS3
PZ70B1	VEGF <sub>165</sub> (-signal seq.)	FPV1
PZ71B1	VEGF165(+signal seq.)	FPV1
PZ115B1	VEGF <sub>121</sub> (+signal seq.)	
PZ116B1	VEGF <sub>121</sub> (-signal seq.)	
PZ72B1	VEGF165-AlaMet-SAP (-signal seq.)	FPVS1
PZ73B1	VEGF165-AlaMet-SAP (+signal seq.)	FPVS1
PZ74B1	SAP-AlaMet-VEGF165	FPSV1
PZ74F5	SAP-AlaMet-VEGF 165	FPSV1

PZ75B1	SAP-(Gly4Ser)4-VEGF165	FPSV2
PZ75F5	SAP-(Gly4Ser)4-VEGF165	FPSV2
PZ76B1	SAP-AlaMet-VEGF121	FPSV3
PZ76F5	SAP-AlaMet-VEGF121	FPSV3
PZ77B1	SAP-G4Sx4-VEGF121	FPSV4
PZ78F5	SAP-G4Sx4-VEGF121	FPSV4
PZ79B1	SAP-AlaMet-VEGF <sub>121</sub> (Gly4Ser)-VEGF <sub>121</sub>	FPSVV1
PZ79F5	SAP-AlaMet-VEGF <sub>121</sub> (GlySer)-VEGF <sub>121</sub>	
PZ80B1	SAP-AlaMet-VEGF121(Gly4Ser)2-VEGF121	FPSVV2
PZ81B1	SAP-AlaMet-VEGF165(Gly4Ser)-VEGF165	FPSVV3
PZ81F5	SAP-AlaMet-VEGF <sub>165</sub> (GlySer)-VEGF <sub>165</sub>	
PZ82B1	SAP-AlaMet-VEGF165(Gly4Ser)2-VEGF165	FPSVV4
PZ83B1	SAP-(Gly4Ser)-VEGF121(Gly4Ser)-VEGF121	FPSVV5
PZ84B1	SAP-(Gly4Ser)2-VEGF121(Gly4Ser)2-	FPSVV6
	VEGF <sub>121</sub>	
PZ85B1	SAP-(Gly4Ser)-VEGF165(Gly4Ser)-VEGF165	FPSVV7
PZ85F5	SAP-(GlySer)-VEGF <sub>165</sub> (Gly4Ser)-VEGF <sub>165</sub>	
PZ86B1	SAP-(Gly4Ser)2-VEGF165(Gly4Ser)2-	FPSVV8
	VEGF <sub>165</sub>	
PZ87I	VEGF <sub>121</sub> (Baculovirus) Viral Stock	FPV2
PZ8717	VEGF <sub>121</sub>	FPV2
PZ88I	VEGF165(Baculovirus) Viral Stock	FPV1
PZ8817	VEGF <sub>165</sub>	FPV1
PZ89I	VEGF121CYS+2(Baculovirus) Viral Stock	FPV3
PZ8917	VEGF <sub>121</sub> CYS+2	FPV3
PZ901	VEGF121CYS+4(Baculovirus) Viral Stock	FPV4
PZ9017	VEGF121CYS+4	FPV4
PZ911	VEGF165CYS+2(Baculovirus) Viral Stock	FPV5
PZ911	VEGF <sub>165</sub> CYS+2	FPV5
PZ921	VEGF165CYS+4 (BACULOVIRUS) Viral	FPV6
PZ92I7	Stock	
PZ93F5	VEGF <sub>165</sub> CYS+4	FPV6
PZ94F5	Met VEGF <sub>121</sub>	FPV2
PZ95B1	Met VEGF <sub>165</sub>	FPVI
PZ96B1	pel B-SAP-AlaMet-V <sub>121</sub> -(G45)-V <sub>121</sub>	FPSVV1
PZ97B1	ompA-SAP-AlaMet-V <sub>121</sub> -(G45)-V <sub>121</sub>	FPSVV1
PZ98B1	ompT-SAP-AlaMet-V <sub>121</sub> -(G45)-V <sub>121</sub>	FPSVV1
PZ99B1	phoA-SAP-AlaMet-V <sub>121</sub> -(G45)-V <sub>121</sub>	FPSVV1
PZ100B1	pelB-SAP-AlaMet-V <sub>165</sub> -(G45)-V <sub>165</sub>	FPSVV3
PZ101B1	ompA-SAP-AlaMet-V <sub>165</sub> -(G45)-V <sub>165</sub>	FPSVV3
PZ102B1	ompT-SAP-AlaMet-V <sub>165</sub> -(G45)-V <sub>165</sub>	FPSVV3
PZ103B1	phoA-SAP-AlaMet-V <sub>165</sub> -(G45)-V <sub>165</sub>	FPSVV3
PZ104B1	SAP-VEGF exon 4.7.8	FPSV5
1210401	SAP-VEGF exon 6.7.8	FPSV7

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PZ105B1	SAP-VEGF exon 3,4,5,6	
PZ106I1	pMAL-p2=I SAP-VEGF exon 3,4,5	FPSV5
PZ107I1	pMAL-p2=1 SAP-VEGF exon 3,4,5,6	FPSV6
PZ108I1	pMAL-p2=I SAP-VEGF exon 6,7,8	FPSV7
PZ111J1	PGEX-SX=SAP VEGF exon 3,4,5	FPSV5
PZ112J1	PGEX-SX=SAP VEGF exon 3,4.5.6	FPSV6
PZ113J1	PGEX-SX=SAP VEGF exon 7.8	FPSV8
PZ114J1	PGEX-SX=SAP VEGF exon 6.7,8	FPSV7

- Details regarding these constructs are described in co-pending U.S. Application Serial Nos. 08/213,446 and 08/213,446, International PCT Application WO 53189, and PCT Appln. US 94/ , filed July 27, 1994
- 5 N/A = not applicable
- The plasmids, such as PZ1A1 are designated with (i) a PZnumber (PZ1), followed by (ii) a letter (A), and optionally (iii) followed by a number (1). The key to these designations: (i) PZnumber - refers to the construct number, (ii) the next letter refers to the plasmid into which the construct was cloned, A=pET 11 without the T7 transcription terminator, B=pET 11 with the T7 transcription terminator, c=pET 13, D=pET 12, E=pET 15b, F=pPL\(\lambda\), G=pKK 223-3, H=PRZ 1 (pKK223-3+Kan<sup>R</sup>), I=pBlueBac III, J=PRZ2 (pKK223-3 + Kan<sup>R</sup> + lacI gene) and (ii) the optional number (or letter) refers to the bacterial strain (number) or insect host (letter) in which the plasmid was introduced, 1=BL21(DE3), 2=BL21(DE3)+pLYS S; 3=HMS174(DE3), 15

4=HMS174(DE3)+pLYS S, 5=N4830(cI8576) and 7=NovaBlue.

A particularly preferred vector for expressing VEGF or VEGF-cytotoxic agent fusion protein is  $pP_L$ - $\lambda$  inducible expression vector (Pharmacia Biotech, Uppsala, Sweden). As described above, this vector contains the tightly regulated leftward promoter of bacterophage  $\lambda$ , which is controlled by the cl repressor. The promoter is temperature inducible in a bacterial host, such as N4830-1, which contains the ts Upon induction, the expressed protein is expressed and repressor cI857. compartmentalized into inclusion bodies. The inclusion bodies are released by lysing the cells, such as with lysozyme digestion and sonication. The insoluble fraction. containing the inclusion bodies, is isolated by centrifugation. The inclusion bodies are solubilized by a strong denaturant, such as 6M guanidine-HCl or urea. The proteins are recovered from the supernatant following centrifugation by dilution into a buffer containing 100mM Tres, 10mM EDTA, 1% monothioglycerol 025M L-arginine. pH9.5. Other equivalent components may be readily substituted as long as the pH is basic and a reduction agent is present. The dilution is performed slowly and the

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mixture stirred for up to 2 hours. Refolding the protein is accomplished by dialysis of the protein into buffer, such as PBS, pH 8.8.

## F. Properties and use of the resulting chemical conjugates and fusion proteins

The conjugates provided herein can be used *in vitro* to identify cells. particularly tumor cells that express receptors to which the conjugate selectively binds and which internalized the conjugates. The cells are contacted with the conjugates and assayed for proliferation. Cells in which proliferation is inhibited express VEGF receptors. If such cells are derived from a tumor, such tumor will be a candidate for treatment with the VEGF conjugate. If such cells are a cell line, such cell line will be useful in drug screening assays for identification of compounds that modulate the activity of VEGF receptors (see, e.g., U.S. Patent Nos. 5.208,145, 5.071,773, 4,981,784, 4,603,106, which describe such assays for other receptors).

# 15 G. Formulation and administration of pharmaceutical compositions

The conjugates herein may be formulated into pharmaceutical compositions suitable for topical, local, intravenous and systemic application. Effective concentrations of one or more of the conjugates are mixed with a suitable pharmaceutical carrier or vehicle. The concentrations or amounts of the conjugates that are effective requires delivery of an amount, upon administration, that ameliorates the symptoms or treats the disease. Typically, the compositions are formulated for single dosage administration. Therapeutically effective concentrations and amounts may be determined empirically by testing the conjugates in known *in vitro* and *in vivo* systems, such as those described here; dosages for humans or other animals may then be extrapolated therefrom.

Upon mixing or addition of the conjugate(s) with the vehicle, the resulting mixture may be a solution, suspension, emulsion or the like. The form of the resulting mixture depends upon a number of factors, including the intended mode of administration and the solubility of the conjugate in the selected carrier or vehicle. The effective concentration is sufficient for ameliorating the symptoms of the disease, disorder or condition treated and may be empirically determined based upon in vitro and/or in vivo data, such as the data from the mouse xenograft model for tumors or rabbit ophthalmic model. If necessary, pharmaceutically acceptable salts or other derivatives of the conjugates may be prepared.

Pharmaceutical carriers or vehicles suitable for administration of the conjugates provided herein include any such carriers known to those skilled in the art to

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be suitable for the particular mode of administration. As used herein, pharmaceutically acceptable salts, esters or other derivatives of the conjugates include any salts, esters or derivatives that may be readily prepared by those of skill in this art using known methods for such derivatization and that produce compounds that may be administered to animals or humans without substantial toxic effects and that either are pharmaceutically active or are prodrugs. A prodrug is a compound that, upon in vivo administration, is metabolized or otherwise converted to the biologically, pharmaceutically or therapeutically active form of the compound. To produce a prodrug, the pharmaceutically active compound is modified such that the active compound will be regenerated by metabolic processes. The prodrug may be designed to alter the metabolic stability or the transport characteristics of a drug, to mask side effects or toxicity, to improve the flavor of a drug or to alter other characteristics or properties of a drug. By virtue of knowledge of pharmacodynamic processes and drug metabolism in vivo, those of skill in this art, once a pharmaceutically active compound is known, can design prodrugs of the compound (see, e.g., Nogrady (1985) Medicinal Chemistry A Biochemical Approach, Oxford University Press, New York, pages 388-392). In addition, the conjugates may be formulated as the sole pharmaceutically active ingredient in the composition or may be combined with other active ingredients.

The conjugates can be administered by any appropriate route, for example, orally, parenterally, intravenously, intradermally, subcutaneously, or topically, in liquid, semi-liquid or solid form and are formulated in a manner suitable for each route of administration. Preferred modes of administration depend upon the indication treated. Dermatological and ophthalmologic indications will typically be treated locally; whereas, tumors and vascular proliferative disorders, will typically be treated by systemic, intradermal, intralesional, or intramuscular modes of administration.

The conjugate is included in the pharmaceutically acceptable carrier in an amount sufficient to exert a therapeutically useful effect in the absence of undesirable side effects on the patient treated. It is understood that number and degree of side effects depends upon the condition for which the conjugates are administered. For example, certain toxic and undesirable side effects are tolerated when treating lifethreatening illnesses, such as tumors, that would not be tolerated when treating disorders of lesser consequence.

The concentration of conjugate in the composition will depend on absorption, inactivation and excretion rates thereof, the dosage schedule, and amount administered as well as other factors known to those of skill in the art.

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As used herein an effective amount of a compound for treating a particular disease is an amount that is sufficient to ameliorate, or in some manner reduce the symptoms associated with the disease. Such amount may be administered as a single dosage or may be administered according to a regimen, whereby it is effective. The amount may cure the disease but, typically, is administered in order to ameliorate the symptoms of the disease. Repeated administration may be required to achieve the desired amelioration of symptoms.

Typically a therapeutically effective dosage should produce a serum concentration of active ingredient of from about 0.1 ng/ml to about 50-100  $\mu$ g/ml. The pharmaceutical compositions typically should provide a dosage of from about 0.01 mg to about 100 - 2000 mg of conjugate, depending upon the conjugate selected, per kilogram of body weight per day. Typically, for intravenous or systemic treatment a daily dosage of about between 0.05 and 0.5 mg/kg should be sufficient. Local application for ophthalmic disorders should provide about 1 ng up to 100  $\mu$ g, preferably about 1  $\mu$ g to about 10  $\mu$ g, per single dosage administration. It is understood that the amount to administer will be a function of the conjugate selected, the indication treated, and possibly the side effects that will be tolerated. Dosages can be empirically determined using recognized models for each disorder.

The active ingredient may be administered at once, or may be divided into a number of smaller doses to be administered at intervals of time. It is understood that the precise dosage and duration of treatment is a function of the disease being treated and may be determined empirically using known testing protocols or by extrapolation from *in vivo* or *in vitro* test data. It is to be noted that concentrations and dosage values may also vary with the severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that the concentration ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed compositions.

Solutions or suspensions used for parenteral, intradermal, subcutaneous, or topical application can include any of the following components: a sterile diluent, such as water for injection, saline solution, fixed oil, polyethylene glycol, glycerine, propylene glycol or other synthetic solvent; antimicrobial agents, such as benzyl alcohol and methyl parabens; antioxidants, such as ascorbic acid and sodium bisulfite; chelating agents, such as ethylenediaminetetraacetic acid (EDTA); buffers, such as acetates, citrates and phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose. Parental preparations can be enclosed in ampules.

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disposable syringes or multiple dose vials made of glass, plastic or other suitable material. If administered intravenously, suitable carriers include physiological saline or phosphate buffered saline (PBS), and solutions containing thickening and solubilizing agents, such as glucose, polyethylene glycol, and polypropylene glycol and mixtures thereof. Liposomal suspensions may also be suitable as pharmaceutically acceptable carriers. These may be prepared according to methods known to those skilled in the art.

The conjugates may be prepared with carriers that protect them against rapid elimination from the body, such as time release formulations or coatings. Such carriers include controlled release formulations, such as, but not limited to, implants and microencapsulated delivery systems, and biodegradable, biocompatible polymers, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, polyorthoesters, polylactic acid and others. These are particularly useful for application to the eye for ophthalmic indications following or during surgery in which only a single administration is possible. Methods for preparation of such formulations are known to those skilled in the art.

The conjugates may be formulated for local or topical application, such as for topical application to the skin and mucous membranes, such as in the eye, in the form of gels, creams, and lotions and for application to the eye or for intracisternal or intraspinal application. Such solutions, particularly those intended for ophthalmic use, may be formulated as 0.01% -10% isotonic solutions, pH about 5-7, with appropriate salts. The ophthalmic compositions may also include additional components, such as hyaluronic acid. The conjugates may be formulated as aerosols for topical application (see, e.g., U.S. Patent Nos. 4,044,126, 4,414,209, and 4,364,923).

If oral administration is desired, the conjugate should be provided in a composition that protects it from the acidic environment of the stomach. For example, the composition can be formulated in an enteric coating that maintains its integrity in the stomach and releases the active compound in the intestine. The composition may also be formulated in combination with an antacid or other such ingredient.

Oral compositions will generally include an inert diluent or an edible carrier and may be compressed into tablets or enclosed in gelatin capsules. For the purpose of oral therapeutic administration, the active compound or compounds can be incorporated with excipients and used in the form of tablets, capsules or troches. Pharmaceutically compatible binding agents and adjuvant materials can be included as part of the composition. When the dosage unit form is a capsule, it can contain, in addition to material of the above type, a liquid carrier such as a fatty oil. In addition, dosage unit forms can contain various other materials which modify the physical form of the dosage unit, for example, coatings of sugar and other enteric agents. The

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conjugates can also be administered as a component of an elixir, suspension, syrup, wafer, chewing gum or the like. A syrup may contain, in addition to the active compounds, sucrose as a sweetening agent and certain preservatives, dyes and colorings and flavors.

The active materials can also be mixed with other active materials that do not impair the desired action, or with materials that supplement the desired action, such as cis-platin for treatment of tumors.

Finally, the compounds may be packaged as articles of manufacture containing packaging material, one or more conjugates or compositions as provided herein within the packaging material, and a label that indicates the indication for which the conjugate is provided.

### H. Therapeutic use of the VEGF conjugates

The conjugates provided herein can be used in pharmaceutical compositions to treat VEGF-mediated pathophysiological conditions by targeting to cells that bear VEGF receptors and inhibiting proliferation of or causing death of the cells. Such pathophysiological conditions include, for example, certain tumors, such as Kaposi's sarcoma, renal cell carcinomas and highly vascularized tumors, rheumatoid arthritis, psoriasis and other hyperproliferative skin disorders. As used herein, a hyperproliferative skin disorder is a disorder that is manifested by a proliferation of endothelial cells of the skin coupled with an underlying vascular proliferation, resulting in a localized patch of scaly, horny or thickened skin or a tumor of endothelial origin. Such disorders include, but are not limited to actinic and atopic dermatitis, toxic eczema, allergic eczema, psoriasis, skin cancers and other tumors, such as Kaposi's sarcoma, angiosarcoma, hemangiomas, and other highly vascularized tumors, and vascular proliferative responses, such as varicose veins. The treatment is effected by administering a therapeutically effective amount of the VEGF conjugate, for example, in a physiologically vehicle suitable for local or systemic application. In particular, for treatment of localized skin disorders the conjugate is formulated for topical, local or intralesional application to the skin and is applied topically, locally or intralesional.

Treatment means any manner in which the symptoms of a conditions, disorder or disease are ameliorated or otherwise beneficially altered. Treatment also encompasses any pharmaceutical use of the compositions herein. Symptoms of a particular disorder are ameliorated by administration of a particular pharmaceutical composition and refers to any lessening, whether permanent or temporary, lasting or transient that can be attributed to or associated with administration of the composition.

The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

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# EXAMPLE 1 RECOMBINANT PRODUCTION OF SAPORIN

#### A. Materials and methods

#### 1. Bacterial Strains

E. coli strain JA221 (lpp hdsM+ trpE5 leuB6 lacY recA1 F'[lacl lacpro+]) is publicly available from the American Type Culture Collection (ATCC), Rockville, MD 20852, under the accession number ATCC 33875. (JA221 is also available from the Northern Regional Research Center (NRRL), Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604, under the accession number NRRL B-15211; see, also, U.S. Patent No. 4,757,013 to Inouye; and Nakamura et al., Cell 18:1109-1117, 1979). Strain INV1α is commercially available from Invitrogen, San Diego, CA.

### 2. DNA Manipulations

20 The restriction and modification enzymes employed herein are commercially available in the U.S. Native saporin and rabbit polyclonal antiserum to saporin were obtained as previously described in Lappi et al., Biochem. Biophys. Res. Comm. 129:934-942. Ricin A chain is commercially available from Sigma, Milwaukee, WI. Antiserum was linked to Affi-gel 10 (Bio-Rad, Emeryville, CA) according to the manufacturer's instructions. Sequencing was performed using the 25 Sequenase kit of United States Biochemical Corporation (version 2.0) according to the Minipreparation and maxipreparation of plasmids. manufacturer's instructions. preparation of competent cells, transformation, M13 manipulation, bacterial media. Western blotting, and ELISA assays were according to Sambrook et al.. (Molecular 30 Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press. Cold Spring Harbor, NY, 1989). The purification of DNA fragments was done using the Geneclean II kit (Bio 101) according to the manufacturer's instructions. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Western blotting was accomplished by transfer of the electrophoresed protein to nitrocellulose using the PhastTransfer system, as described by the manufacturer. The antiserum to SAP was used at a dilution of 1:1000. Horseradish peroxidase labeled anti-IgG was used as the second antibody (see Davis et al., Basic

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Methods In Molecular Biology, New York, Elsevier Science Publishing Co., pp 1-338, 1986).

### B. Isolation of DNA encoding saporin

## Isolation of genomic DNA and preparation of polymerase chain reaction (PCR) primers

Saponaria officinalis leaf genomic DNA was prepared as described in Bianchi et al., Plant Mol. Biol. 11:203-214, 1988. Primers for genomic DNA amplifications were synthesized in a 380B automatic DNA synthesizer. The primer corresponding to the "sense" strand of saporin (SEQ ID NO. 1) includes an EcoR 1 restriction site adapter immediately upstream of the DNA codon for amino acid -15 of the native saporin N-terminal leader sequence (SEQ ID NO. 1):

5'-CTGCAGAATTCGCATGGATCCTGCTTCAAT-3'.

The primer 5'-CTGCAGAATTCGCCTCGTTTGACTACTTTG-3' (SEQ ID NO. 2) corresponds to the "antisense" strand of saporin and complements the coding sequence of saporin starting from the last 5 nucleotides of the DNA encoding the carboxyl end of the mature peptide. Use of this primer introduced a translation stop codon and an *EcoRI* restriction site after the sequence encoding mature saporin.

## 20 2. Amplification of DNA encoding saporin

Unfractionated Saponaria officinalis leaf genomic DNA (1 µl) was mixed in a final volume of 100 µl containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl. 0.01% gelatin, 2 mM MgCl<sub>2</sub>, 0.2 mM dNTPs, 0.8 µg of each primer. Next, 2.5 U Taql DNA polymerase (Perkin Elmer Cetus) was added and the mixture was overlaid with 30 µl of mineral oil (Sigma). Incubations were done in a DNA Thermal Cycler (Ericomp). One cycle included a denaturation step (94°C for 1 min.), an annealing step (60°C for 2 min.), and an elongation step (72°C for 3 min.). After 30 cycles, a 10 µl aliquot of each reaction was run on a 1.5% agarose gel to verify the correct structure of the amplified product.

The amplified DNA was digested with *EcoRI* and subcloned into *EcoR* I-restricted M13mp18 (see, Yanisch-Perron et al. (1985). Gene 33:103). Single-stranded DNA from recombinant phages was sequenced using oligonucleotides based on internal points in the coding sequence of saporin (see. Bennati et al., Eur. J. Biochem. 183:465-470, 1989). Nine of the M13mp18 derivatives were sequenced and compared. Of the nine sequenced clones, five had unique sequences, set forth as SEQ ID NOS. 3-7, respectively. The clones were designated M13mp18-G4. -G1. -G2. -G7.

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and -G9. Each of these clones contains all of the saporin coding sequence and 45 nucleotides of DNA encoding the native saporin N-terminal leader peptide.

### C. pOMPAG4 Plasmid Construction

M13 mp18-G4, containing the SEQ ID NO. 3 clone from Example 1.B.2., was digested with EcoR I, and the resulting fragment was ligated into the EcoR I site of the vector pIN-IIIompA2 (see, e.g., see, U.S. Patent No. 4,575,013 to Inouye; and Duffaud et al., Meth. Enz. 153:492-507, 1987) using the methods described in Example 1.A.2. The ligation was accomplished such that the DNA encoding saporin, including the N-terminal extension, was fused to the leader peptide segment of the bacterial ompA gene. The resulting plasmid pOMPAG4 contains the lpp promoter (Nakamura et al., Cell 18:1109-1117, 1987), the E. coli lac promoter operator sequence (lac O) and the E. coli ompA gene secretion signal in operative association with each other and with the saporin and native N-terminal leader-encoding DNA listed in SEQ ID NO. 3. The plasmid also includes the E. coli lac repressor gene (lac I).

The M13 mp18-G1, -G2, -G7, and -G9 clones obtained from Example 1.B.2, containing SEQ ID NOS. 4-7 respectively, are digested with *EcoR* I and ligated into *EcoR* I digested pIN-IIIompA2 as described for M13 mp18-G4 above in this example. The resulting plasmids, labeled pOMPAG1, pOMPAG2, pOMPAG7, pOMPA9, are screened, expressed, purified, and characterized as described for the plasmid pOMPAG4.

INV1a competent cells were transformed with pOMPAG4 and cultures containing the desired plasmid structure were grown further in order to obtain a large preparation of isolated pOMPAG4 plasmid using methods described in Example 1.A.2.

### D. Saporin expression in E. coli

The pOMPAG4 transformed *E. coli* cells were grown under conditions in which the expression of the saporin-containing protein is repressed by the lac repressor until the end of log phase of growth after which IPTG was added to induce expression of the saporin-encoding DNA.

To generate a large-batch culture of pOMPAG4 transformed *E. coli* cells, an overnight culture (lasting approximately 16 hours) of JA221 *E. coli* cells transformed with the plasmid pOMPAG4 in LB broth (see e.g., Sambrook et al., supra) containing 125 mg/ml ampicillin was diluted 1:100 into a flask containing 750 ml LB broth with 125 mg/ml ampicillin. Cells were grown at logarithmic phase shaking at 37° C until the optical density at 550 nm reached 0.9 measured in a spectrophotometer.

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In the second step, saporin expression was induced by the addition of IPTG (Sigma) to a final concentration of 0.2 mM. Induced cultures were grown for 2 additional hours and then harvested by centrifugation (25 min.,  $6500 \times g$ ). The cell pellet was resuspended in ice cold 1.0 M TRIS, pH 9.0, 2 mM EDTA (10 ml were added to each gram of pellet). The resuspended material was kept on ice for 20-60 minutes and then centrifuged (20 min.,  $6500 \times g$ ) to separate the periplasmic fraction of *E. coli*, which corresponds to the supernatant, from the intracellular fraction corresponding to the pellet.

## 10 E. Purification of secreted recombinant saporin

## 1. Anti-SAP immuno-affinity purification

The periplasmic fraction from Example 1.D. was dialyzed against borate-buffered saline (BBS: 5 mM boric acid, 1.25 mM borax, 145 mM sodium chloride, pH 8.5). The dialysate was loaded onto an immunoaffinity column (0.5 x 2 cm) of anti-saporin antibodies, obtained as described in Lappi et al., *Biochem. Biophys. Res. Comm.*, 129:934-942, 1985, bound to Affi-gel 10 and equilibrated in BBS at a flow rate of about 0.5 ml/min. The column was washed with BBS until the absorbance at 280 nm of the flow-through was reduced to baseline. Next the column containing the antibody bound saporin was eluted with 1.0 M acetic acid and 0.5 ml fractions were collected in tubes containing 0.3 ml of 2 M ammonium hydroxide. pH 10. The fractions were analyzed by ELISA (see, e.g., Sambrook et al., supra). The peak fraction of the ELISA was analyzed by Western blotting as described in Example 1.A.2 and showed a single band with a slightly higher molecular weight than native saporin. The fractions that contained saporin protein, as determined by the ELISA, were then pooled for further purification.

# 2. Reverse phase high performance liquid chromatography purification

To further purify the saporin secreted into the periplasm, the pooled fractions from Example 1.E.1. were diluted 1:1 with 0.1% trifluoroacetic acid (TFA) in water and chromatographed in reverse phase high pressure liquid chromatography (HPLC) on a Vydac C4 column (Western Analytical) equilibrated in 20% acetonitrile. 0.1% TFA in water. The protein was eluted with a 20 minute gradient to 60% acetonitrile. The HPLC produced a single peak that was the only area of immunoreactivity with anti-SAP antiserum when analyzed by a western blot as described in Example 1.E.1. Samples were assaved by an ELISA.

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Sequence analysis was performed by Edman degradation in a gas-phase sequenator (Applied Biosystems) (see, e.g., Lappi et al., Biochem. Biophys. Res. Comm. 129:934-942, 1985). The results indicated that five polypeptides were obtained that differ in the length, between 7 and 12 amino acids, of the N-terminal saporin leader before the initial amino acid valine of the mature native saporin (SEQ ID NO.3: residue -12 through -7). All of the N-terminal extended variants retained cytotoxic activity. The size of the native leader is 18 residues, indicating that the native signal peptide is not properly processed by bacterial processing enzymes. The ompA signal was, however, properly processed.

To obtain homogeneous saporin, the recombinantly produced saporin can be separated by size.

#### F. Purification of intracellular soluble saporin

To purify the cytosolic soluble saporin protein, the pellet from the intracellular fraction of Example 1.E. above was resuspended in lysis buffer (30 mM 15 TRIS, 2 mM EDTA, 0.1% Triton X-100, pH 8.0, with 1 mM PMSF, 10 µg/ml pepstatin A, 10 µg aprotinin, 10 µg/ml leupeptin and 100 µg/ml lysozyme, 3.5 ml per gram of original pellet). To lyse the cells, the suspension was left at room temperature for one hour, then frozen in liquid nitrogen and thawed in a 37°C bath three times, and 20 then sonicated for two minutes. The lysate was centrifuged at 11,500 x g for 30 min. The supernatant was removed and stored. The pellet was resuspended in an equal volume of lysis buffer, centrifuged as before, and this second supernatant was combined with the first. The pooled supernatants were dialyzed versus BBS and chromatographed over the immunoaffinity column as described in Example 1.E.1. This material also retained cytotoxic activity.

#### G. Assay for cytotoxic activity

The RIP activity of recombinant saporin was compared to the RIP activity of native SAP in an in vitro assay measuring cell-free protein synthesis in a nuclease-treated rabbit reticulocyte lysate (Promega). Samples of immunoaffinitypurified saporin, obtained in Example 1.E.1., were diluted in PBS and 5 µl of sample was added on ice to 35 µl of rabbit reticulocyte lysate and 10 µl of a reaction mixture containing 0.5 µl of Brome Mosaic Virus RNA, 1 mM amino acid mixture minus leucine, 5 µCi of tritiated leucine and 3 µl of water. Assay tubes were incubated 1 hour in a 30°C water bath. The reaction was stopped by transferring the tubes to ice and adding 5 µl of the assay mixture, in triplicate, to 75 µl of 1 N sodium hydroxide, 2.5% hydrogen peroxide in the wells of a Millititer HA 96-well filtration plate (Millipore).

When the red color had bleached from the samples, 300 µl of ice cold 25% trichloroacetic acid (TCA) were added to each well and the plate left on ice for another 30 min. Vacuum filtration was performed with a Millipore vacuum holder. The wells were washed three times with 300 µl of ice cold 8% TCA. After drying, the filter paper circles were punched out of the 96-well plate and counted by liquid scintillation techniques.

The IC<sub>50</sub> for the recombinant and native saporin were approximately 20 pM. Therefore, recombinant saporin-containing protein has full protein synthesis inhibition activity when compared to native saporin.

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## EXAMPLE 2 RECOMBINANT PRODUCTION OF FGF-SAP FUSION PROTEIN

## General Descriptions

## 1. Bacterial Strains and Plasmids:

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS were purchased from Novagen, Madison, WI. Plasmid pFC80, described below, has been described in the PCT Application No. WO 90/02800, except that the bFGF coding sequence in the plasmid designated pFC80 herein has the sequence set forth as SEQ ID NO. 12, nucleotides 1-465. The plasmids described herein may be prepared using pFC80 as a starting material or, alternatively, by starting with a fragment containing the cII ribosome binding site (SEQ ID NO. 15) linked to the FGF-encoding DNA (SEQ ID NO. 12).

E. coli strain JA221 (lpp hdsM+ trpE5 leuB6 lacY recA1 F'[lacl lac pro]) is publicly available from the American Type Culture Collection (ATCC), Rockville, MD 20852, under the accession number ATCC 33875. (JA221 is also available from the Northern Regional Research Center (NRRL), Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604, under the accession number NRRL B-15211; see. also, U.S. Patent No. 4,757,013 to Inouye; and Nakamura et al., Cell 18:1109-1117, 1979). Strain INV1α is commercially available from Invitrogen. San Diego, CA.

### 2. DNA Manipulations

Native SAP, chemically conjugated bFGF-SAP and rabbit polyclonal antiserum to SAP and FGF were obtained as described in Lappi et al., Biochem. Biophys. Res. Comm. 129:934-942, 1985, and Lappi et al., Biochem. Biophys., Res. Comm. 160:917-923, 1989. The pET System Induction Control was purchased from

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Novagen, Madison, WI. The sequencing of the different constructions was done using the Sequenase kit of United States Biochemical Corporation (version 2.0). Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (see, e.g., Sambrook et al., supra). The purification of DNA fragments was done using the Geneclean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Rabbit polyclonal antiserum to SAP and FGF were obtained as described in Lappi et al., *Biochem. Biophys. Res. Comm. 129*:934-942, 1985, and Lappi et al., *Biochem. Biophys.. Res. Comm. 160*:917-923, 1989. The pET System Induction Control was purchased from Novagen, Madison, WI. Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (*see*, *e.g.*, Sambrook et al., supra). The purification of DNA fragments was done using the Geneclean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Western blotting was accomplished by transfer of the electrophoresed protein to nitrocellulose using the PhastTransfer system, as described by the manufacturer. Horseradish peroxidase labeled anti-IgG was used as the second antibody (see Davis et al., Basic Methods In Molecular Biology, New York, Elsevier Science Publishing Co., pp. 1-338, 1986).

### B. Construction of plasmids encoding FGF-SAP fusion proteins

# Construction of FGFM13 that contains DNA encoding the CI ribosome binding site linked to FGF

A NcoI restriction site was introduced into the SAP-encoding DNA the M13mp18-G4 clone, prepared as described in Example 1.B.2. by site-directed mutagenesis method using the Amersham in vitro-mutagenesis system 2.1. The oligonucleotide employed to create the Nco I restriction site was synthesized using a 380B automatic DNA synthesizer (Applied Biosystems) and is listed as:

SEQ ID NO. 8 - CAACAACTGCCATGGTCACATC.

This oligonucleotide containing the *Nco* I site replaced the original SAP-containing coding sequence at SEQ ID NO.3, nts 32-53. The resulting M13mp18-G4 derivative is termed mpNG4.

In order to produce a bFGF coding sequence in which the stop codon was removed, the FGF-encoding DNA was subcloned into a M13 phage and subjected to site-directed mutagenesis. Plasmid pFC80 is a derivative of pDS20 (see. e.g.,

Duester et al., Cell 30:855-864, 1982; see, also, U.S. Patent Nos. 4,914,027, 5,037,744, 5,100,784, and 5,187,261; see, also, PCT Application No. WO 90/02800; and European Patent Application No. EP 267703 A1), which is almost the same as plasmid pKG1800 (see, Bernardi et al., DNA Sequence 1:147-150, 1990; see, also, McKenney et al. (1981) pp. 383-415 in Gene Amplification and Analysis 2: Analysis of Nucleic Acids by Enzymatic Methods, Chirikjian et al. (eds.), North Holland Publishing Company. Amsterdam) except that it contains an extra 440 bp at the distal end of galK between nucleotides 2440 and 2880 in pDS20. Plasmid pKG1800 includes the 2880 bp EcoR 1-Pvu II of pBR322 that contains the contains the ampicillin resistance gene and an origin of replication.

Plasmid pFC80 was prepared from pDS20 by replacing the entire galK gene with the FGF-encoding DNA of SEQ ID NO. 12, inserting the trp promoter (SEQ ID NO. 14) and the bacteriophage lambda cII ribosome binding site (SEQ. ID No. 15: see, e.g., Schwarz et al., Nature 272:410, 1978) upstream of and operatively linked to the FGF-encoding DNA. The trp promoter can be obtained from plasmid pDR720 (Pharmacia PL Biochemicals) or synthesized according to SEQ ID NO. 14. Plasmid pFC80, contains the 2880 bp EcoRI-BamHI fragment of plasmid pSD20, a synthetic Sal I-Nde I fragment that encodes the Trp promoter region (SEQ ID NO. 14):

EcoR 1

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AATTCCCCTGTTGACAATTAATCATCGAACTAGTTAACTAGTACGCAGCTTGGCTGCAG and the cII ribosome binding site (SEQ ID NO. 15)):

Sal I Nde I
GTCGACCAAGCTTGGGCATACATTCAATCAATTGTTATCTAAGGAAATACTTACATATG

The FGF-encoding DNA was removed from pFC80 by treating it as follows. The pFC80 plasmid was digested by Hga I and Sal I, which produces a fragment containing the cII ribosome binding site linked to the FGF-encoding DNA. The resulting fragment was blunt ended with poll (Klenow's fragment) and inserted into M13mp18 that had been opened by Sma I and treated with alkaline phosphatase for blunt-end ligation. In order to remove the stop codon, an insert in the ORI minus direction was mutagenized, as described above, using the following oligonucleotide (SEQ ID NO. 9): GCTAAGAGCGCCATGGAGA. SEQ ID NO. 9 contains one nucleotide between the FGF carboxy terminal serine codon and a Nco I restriction site: it replaced the following wild type FGF encoding DNA having SEQ ID NO. 10:

GCT AAG AGC TGA CCA TGG AGA Ala Lys Ser STOP Pro Trp Arg

The resulting mutant derivative of M13mp18, lacking a native stop codon after the carboxy terminal serine codon of bFGF, was designated FGFM13. The mutagenized region of FGFM13 contained the correct sequence (SEQ ID NO. 11).

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# 2. Preparation of plasmids pFS92 (PZ1A), PZ1B and PZ1C that encode the FGF-SAP fusion protein (FPFS1)

## a. Plasmid pFS92 (also designated PZ1A)

Plasmid FGFM13 was cut with *Nco* I and *Sac* I to yield a fragment containing the cII ribosome binding site linked to the bFGF coding sequence with the stop codon replaced.

The M13mp18 derivative mpNG4 containing the saporin coding sequence was also cut with restriction endonucleases *Nco* I and *Sac* I, and the bFGF coding fragment from FGFM13 was inserted by ligation to DNA encoding the fusion protein bFGF-SAP into the M13mp18 derivative to produce mpFGF-SAP, which contains the cII ribosome binding site linked to the FGF-SAP fusion gene. The sequence of the fusion gene is set forth in SEQ ID NO. 12 and indicates that the FGF protein carboxy terminus and the saporin protein amino terminus are separated by 6 nucleotides (SEQ ID NOS. 12 and 13, nts 466-471) that encode two amino acids Ala Met.

Plasmid mpFGF-SAP was digested with Xba I and EcoR I and the resulting fragment containing the bFGF-SAP coding sequence was isolated and ligated into plasmid pET-11a (available from Novagen, Madison, WI; for a description of the plasmids see U.S. Patent No. 4,952,496; see, also. Studier et al., Meth. Enz. 185:60-89, 1990; Studier et al., J. Mol. Biol. 189:113-130, 1986; Rosenberg et al., Gene 56:125-135, 1987) that had also been treated with EcoR I and Xba I. The resulting plasmid was designated pFS92. It was renamed PZ1A.

Plasmid pFS92 (or PZ1A) contains DNA the entire basic FGF protein (SEQ ID NO. 12), a 2-amino acid long connecting peptide, and amino acids 1 to 253 of the mature SAP protein. Plasmid pFS92 also includes the cII ribosome binding site linked to the FGF-SAP fusion protein and the T7 promoter region from pET-11a.

E. coli strain BL21(DE3)pLysS (Novagen. Madison WI) was transformed with pFS92 according to manufacturer's instructions and the methods described in Example 2.A.2.

### b. Plasmid PZ1B

Plasmid pFS92 was digested with EcoR I, the ends repaired by adding nucleoside triphosphates and Klenow DNA polymerase, and then digested with Nde I to release the FGF-encoding DNA without the cII ribosome binding site. This fragment was ligated into pET 11a, which had been BamH I digested, treated to repair the ends.

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and digested with Nde I. The resulting plasmid was designated PZ1B. PZ1B includes the T7 transcription terminator and the pET-11a ribosome binding site.

E. coli strain BL21(DE3) (Novagen, Madison WI) was transformed with PZ1B according to manufacturer's instructions and the methods described in Example 2.A.2.

#### c. Plasmid PZ1C

Plasmid PZ1C was prepared from PZ1B by replacing the ampicillin resistance gene with a kanamycin resistance gene.

#### d. Plasmid PZ1D

Plasmid pFS92 was digested with EcoR I and Nde I to release the FGF-encoding DNA without the cII ribosome binding site and the and the ends were repaired. This fragment was ligated into pET 12a, which had been BamH I digested and treated to repair the ends. The resulting plasmid was designated PZ1D. PZ1D includes DNA encoding the ompT secretion signal operatively linked to DNA encoding the fusion protein.

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS (Novagen, Madison WI) were transformed with PZ1D according to manufacturer's instructions and the methods described in Example 2.A.2.PZM417V2

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## EXAMPLE 3 PREPARATION OF MODIFIED SAPORIN

Saporin was modified by addition of a cysteine residue at the N-terminus-encoding portion of the DNA or by the addition of a cysteine at position 4 or 10. The resulting saporin is then reacted with an available cysteine on an FGF to produce conjugates that are linked via the added Cys or Met-Cys on saporin.

Modified SAP has been prepared by altering the DNA encoding the SAP by inserting DNA encoding Met-Cys at position -1 or by replacing the Ile or the Asp codon within 10 or fewer residues of the N-terminus with Cys. The resulting DNA has been inserted into pET 11a and pET 15b and expressed in BL21(DE3) cells. The resulting saporin proteins are designated FPS1 (saporin with Cys at -1), FPS2 (saporin with Cys at position 4) and FPS3 (saporin with Cys at position 10). A plasmid that encodes FPS1 and that has been used for expression of FPS1 has been designated PZ50B. Plasmids that encode FPS2 and that have been used for expression of FPS2 have been designated PZ51B (pET11a-based plasmid) and PZ51E (pET15b-based

plasmid). Plasmids that encode FPS3 and that have been used for expression of FPS3 have been designated PZ52B (pET11a-based plasmid) and PZ52E (pET 15b-based plasmid).

#### 5 A. Materials and Methods

#### 1. Bacterial strains

Novablue (Novagen, Madison, WI) and BL21(DE3) (Novagen, Madison WI).

## 10 2. DNA manipulations

DNA manipulations were performed as described in Examples 1 and 2. Plasmid PZ1B (designated PZ1B1 (the "1" at the end refers to the bacterial host strain. BL21(DE3)) described in Example 2 was used as the DNA template.

## 15 B. Preparation of saporin with an added cysteine residue at the N-terminus

The DNA encoding SAP-6 was amplified by polymerase chain reaction (PCR) from the parental plasmid pZ1B1 as described by McDonald et al. (1995). The plasmid pZ1B1 contains the DNA sequence for human FGF-2 linked to SAP-6 by a two amino acid linker (Ala-Met). pZ1B1 also includes the T7 promoter, lac operator, 20 ribosomal binding site, and T7 terminator present in the pET-11a vector. For SAP-6 amplification, the 5' primer (5' CATATGTGTGTCACATCAATCAC ATTAGAT-3') (SEQ. ID No. 34) corresponding to the "sense" strand of SAP-6 incorporated a Ndel restriction enzyme site used for cloning. It also contained a Cys codon at position -1 relative to the start site of the mature protein sequence. No leader sequence was included. The 3' primer (5' CAGGTTTGGATCCTTTACGTT 3') (SEO. ID No. 35), corresponding to the "antisense" strand of SAP-6 has a BamHl site used for cloning. The amplified DNA was gel purified and digested with Ndel and BamHI. The digested SAP-6 DNA fragment was subcloned into the NdeI and BamHI digested pZ1B1. This digestion removed FGF-2 and the 5' portion of SAP-6 (up to nucleotide position 650) from the parental rFGF2-SAP vector (pZ1B1) and replaced this portion with a SAP-6 molecule containing a Cys at position -1 relative to the start site of the native mature SAP-6 protein. The resultant plasmid was designated as pZ50B. pZ50B was transformed into E. coli strain NovaBlue for restriction and sequencing analysis. The appropriate clone was then transformed into E. coli strain BL21(DE3) for 35 expression and large scale production.

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# C. Preparation of saporin with a cysteine residue at position 4 or 10 of the native protein

These constructs were designed to introduce a cysteine residue at position 4 or 10 of the native protein by replacing the isoleucine residue at position 4 or the asparagine residue at position 10 with cysteine.

SAP was amplified by polymerase chain reaction (PCR) from the parental plasmid pZ1B encoding the FGF-SAP fusion protein using a primer corresponding to the sense strand of saporin, spanning nucleotides 466-501 of SEQ ID NO. 12, which incorporates a *NdeI* site and replaces the Ile codon with a Cys codon at position 4 of the mature protein (SEQ ID NO. 69):

CATATGGTCACATCATGTACATTAGATCTAGTAAAT.

or a primer corresponding to the sense strand of saporin, nucleotides 466-515 of SEQ ID NO. 12, incorporates a *Ndel* site and replaces the Asp codon with a Cys codon at position 10 of the mature protein (SEQ ID NO. 70)

15 CATATGGTCACATCACATTAGATCTAGTATGTCCGACCGCGGGTCA. The 3' primer complements the coding sequence of saporin spanning nucleotides 547-567 of SEQ ID NO. 12 and contains a BamHI site (SEQ ID NO. 35):

## CAGGTTTGGATCCTTTACGTT.

using the following cycles: denaturation step 94°C for 1 min, annealing for 2 min at 60°C, and extension for 2 min at 72°C for 35 cycles. The amplified DNA was gel purified, digested with Ndel and BamHI, and subcloned into Ndel and BamHI digested pZ1B. This digestion removed the FGF and 5' portion of SAP (up to the BamHI site) from the parental FGF-SAP vector (pZ1B) and replaced this portion with a SAP molecule containing a Cys at position 4 or 10 relative to the start site of the native mature SAP protein (see SEQ ID NOs. 29 and 30, respectively). The resulting plasmids are designated pZ51B and pZ52B, respectively.

## D. Cloning of DNA encoding SAP mutants in vector pET15b

## 1. The SAP-Cys-1 mutants

The initial step in this construction was the mutagenesis of the internal BamHI site at nucleotides 555-560 (SEQ ID NO. 12) in pZ1B by PCR using a sense primer corresponding to nucleotides 543-570 (SEQ ID NO. 12) but changing the G at nucleotide 555 (the third position in the Lys codon) to an A. The complement of the sense primer was used as the antisense primer (SEQ ID NO. 73). The first round of amplification used primers SEQ ID NOs. 34 and 73 or 37 and 74 conducted as in B above. Individual fragments were gel purified and a second round of amplification was

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performed using primers of SEQ ID Nos. 34 and 74 as in B, above. This amplification introduced a *NdeI* site and a Cys codon onto the 5' end of the saporin-encoding DNA. The antisense primer was complementary to the 3' end of the saporin protein and encoded a *BamHI* site for cloning and a stop codon (SEQ ID NO. 37):

GGATCCGCCTCGTTTGACTACTT.

The resulting fragment was digested with Ndel/BamHI and inserted into pET15b (Novagen, Madison, WI), which has a His-Tag<sup>TM</sup> leader sequence (SEQ ID NO. 36), that had also been digested with Ndel/BamHI.

#### 2. The SAP-Cys+4 and Sap-Cys+10 mutants

This construction was performed similarly to the SAP-Cys-1 using pZ1B as the starting material, and splice overlap extension (SOE) using PZ1B as the starting plasmid, including mutagenesis of the internal *BamHI* site at nucleotides 555-560 (SEQ ID NO. 12) in pZ1B by PCR using a sense primer corresponding to nucleotides 543-570 (SEQ ID NO. 12) but changing the G at nucleotide 555 (the third position in the Lys codon) to an A and introduction of the cys at position 4 or 10 in place of the native amino acid.

The first round of amplification used primers of SEQ ID NOs. 69 and 73 (for the cys+4 saporin mutants) or SEQ ID NOs. 70 and 73 for the cys+10 saporin mutants):

CATATGGTCACATCATGTACATTAGATCTAGTAAAT (SEQ ID NO. 69);
CATATGGTCACATCACATTAGATCTAGTATGTCCGACCGCGGGTCA (SEQ ID NO. 70);
TTTCAGGTTTGGATCTTTTACGTTGTTT (SEQ ID NO. 73).

Amplification conditions were as follows: denaturation for 1 min at 94°C, annealing for 2 min at 70°C and extension for 2 min at 72°C for 35 cycles. Individual fragments were gel purified and subjected to a second round of amplification, following the same protocol, using only the external oligos of SEQ ID NO. 37 and SEQ ID NO. 69 for the cys+4 mutant or SEQ ID NO. 70 for the cys+10 mutant. The resulting fragments had a NdeI site on the 5' end of the saporin-encoding DNA and a BamHI site for cloning and a stop codon on the 3' end. The resulting fragment was digested with NdeI/BamHI and inserted into pET 15b (Novagen. Madison, WI), which has a His-Tag<sup>TM</sup> leader sequence (SEQ ID NO. 36), that had also been digested NdeI/BamHI.

DNA encoding unmodified SAP (EXAMPLE 1) can be similarly inserted into a pET15b or pET11a and expressed as described below for the modified SAP-encoding DNA.

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## E. Expression of the modified saporin-encoding DNA

The E. coli cells containing Cys-1 SAP construct were grown in a high cell density fed-batch fermentation with the temperature and pH controlled at 30°C and 6.9, respectively. A glycerol stock (1 mL) was grown in 50 ml of Luria Broth until A<sub>600</sub> reached 0.6. Inoculum (10 mL) was injected into a 7 L Applikon (Foster City, CA) fermentor containing 2 L of complex batch media consisting of 5 g/L of glucose, 1.25 g/L, each, of yeast extract and tryptone (Difco Laboratories, Detroit, MI, U.S.A.), 7 g/L of K<sub>2</sub>HPO<sub>4</sub>, 8 g/L of KH<sub>2</sub>PO<sub>4</sub>, 1.66 g/L of (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 1 g/L of MgSO<sub>4</sub>•7H<sub>2</sub>O, 2 mL/L of a trace metal solution (74 g/L of Na<sub>3</sub>Citrate, 27 g/L of FeCl<sub>3</sub>•6H<sub>2</sub>O, 2.0 g/L of  $CoCl_2•6H_2O$ ,  $2.0 \, g/L$  of  $Na_2MoO_4•2H_2O$ ,  $1.9 \, g/L$  of  $CuSO_4•5H_2O$ ,  $1.6 \, g/L$  of MnCl<sub>2</sub>•4H<sub>2</sub>O, 1.4 g/L of ZnCl<sub>2</sub>•4H<sub>2</sub>O, 1.0 g/L of CaCl<sub>2</sub>•2H<sub>2</sub>O, 0.5 g/L of H<sub>3</sub>BO<sub>3</sub>), 2 mL/L of a vitamin solution (6 g/L thiamine+HCl, 3.05 g/L of niacin, 2.7 g/L of pantothenic acid, 0.7 g/L of pyridoxine•HCl, 0.21 g/L of riboflavin, 0.03 g/L of biotin, 0.02 g/L of folic acid), and 100 mg/L of carbenicillin. The culture was grown for 12 hour before initiating the continuous addition of a 40x solution of complex batch media lacking the phosphates and containing only 25 mL/L, each, of trace metal and vitamin solutions. The feed addition continued until the A<sub>600</sub> of the culture reached 85, at which time (approximately 9 h) the culture was induced with 0.1 mM IPTG. During 4 h of post-induction incubation, the culture was fed with a solution containing 100 g/L of glucose, 100 g/L of yeast extract, and 200 g/L of tryptone. Finally, the cells were harvested by centrifugation (8,000 x g, 10 min) and frozen at -80°C until further processed.

## F. Purification and conjugation of modified saporin

The cell pellet (~400 g wet weight) containing Cys-1 SAP was resuspended in 3 volumes of buffer B (10 mM sodium phosphate, pH 7.0, 5 mM EGTA, and 1 mM DTT). The suspension was passed through a microfluidizer three times at 18,000 lb/in<sup>2</sup> on ice. The resultant lysate was diluted with NanoPure H<sub>2</sub>O until conductivity fell below 2.7 mS/cm. All subsequent procedures were performed at room temperature.

The dilute lysate was loaded onto an expanded bed of Streamline SP cation-exchange resin (300 ml) pre-equilibrated with buffer C (20 mM sodium phosphate, pH 7.0, 1 mM EDTA) at 100 mL/min upwards flow. The resin was washed with buffer C until it appeared clear. The plunger was then lowered at 2 cm/min while washing continued at 70 mL/min. Upwards flow was stopped when the plunger was approximately 8 cm away from the bed, and the plunger was allowed to move to within 0.5 cm of the packed bed. The resin was further washed at 70 mL/min downwards flow

until  $A_{280}$  reached baseline. Buffer C plus 0.25 M NaC1 was then used to elute proteins containing Cys-1 SAP at the same flow rate.

The eluate was buffer exchanged into buffer D (50 mM sodium borate, pH 8.5, 1 mM EDTA) using the Sartocon Mini crossflow filtration system with a 10,000 NMWCO module (Sartorious, Goettingen, Germany). The sample was then applied to a column of Source 15S (30 mL) pre-equilibrated with buffer D. A 10 column volume linear gradient of 0 to 0.3 M NaC1 in buffer D was used to elute Cys-1 SAP at 30 mL/min.

Both Cys-1 SAP and C96S FGF-2 were reduced with a final concentration of 10 mM DTT prior to gel filtration with buffer E (0.1 M sodium phosphate, pH 7.5, 0.1 M NaC1, 1 mM EDTA). The Cys-1 SAP was then reacted with 80-fold molar excess of DTNB at room temperature for 1 h, and the amount of Cys-1 SAP-TNB was determined by measuring absorbance at 412 nm using the molar absorption coefficient of 14,150 M<sup>-1</sup>cm<sup>-1</sup>. The Cys-1 SAP/DTNB mixture was subjected to size exclusion chromatography and eluted with buffer E. The C96S FGF-2 was added to the DTNB-treated Cys-1 SAP in a molar ratio of 3:1, and the reaction was carried out at 4°C overnight.

The reaction mixture was loaded onto a column of Heparin-Sepharose CL-4B pre-equilibrated with 0.5 M NaC1 in buffer F (10 mM sodium phosphate, pH 6.0, 1 mM EDTA). The column was washed with 0.5 M then 1 MNaC1 in buffer F, and the conjugate eluted with 2 M NaC1 in buffer F. Fractions containing FGF2-Cys-1 SAP were combined, concentrated, and applied to a column of Superdex 75. Buffer G (10 mM sodium phosphate, pH 6.0, 0.15 M NaC1, 0.1 mM EDTA) was used for the Superdex 75 column.

During Cys-1 SAP purification, SDS-PAGE was performed on 12% acrylamide Mini-PROTEAN II Ready Gels (Bio-Rad, Hercules, CA, U.S.A.) according to the method of Laemmli (1970) under non-reducing conditions. PhastSystem using 10-15% acrylamide gradient gels.

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#### **EXAMPLE 4**

PRODUCTION OF VEGF, VEGF-SAP AND SAP-VEGF CONSTRUCTS

#### A. General Descriptions

#### 1. Bacterial Strains and Plasmids:

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS were purchased from Novagen. Madison. WI.

#### 2. DNA Manipulations

Native SAP and rabbit polyclonal antiserum to SAP were obtained as described above or as described in Lappi et al. (1985) Biochem. Biophys. Res. Comm., 129:934-942 and Lappi et al. (1989) Biochem. Biophys., Res. Comm., 160:917-923. The pET System Induction Control was purchased from Novagen, Madison, WI. The sequencing of the different constructions was done using the Sequenase kit of United States Biochemical Corporation (version 2.0). Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (see, e.g., Sambrook et al. (1989) Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The purification of DNA fragments was done using the Geneclean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

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#### 3. Materials:

Bacterial strains: Novablue and BL21(DE3) (Novagen, Madison, WI). Constructs that have been prepared include:

VEGF165:SAP containing the VEGF leader sequence (amino

20 acids 1-26; see, e.g., SEQ ID NO. 26);

VEGF165:SAP without the leader sequence;

SAP: VEGF165 containing the VEGF leader sequence;

SAP:VEGF165 without the leader sequence;

VEGF165 containing the leader sequence; and

VEGF165 without the leader sequence; and similar constructs with VEGF<sub>121</sub> (see also Table 3).

Constructs containing any of VEGF121. VEGF189 and VEGF206 in place of VEGF165 are prepared in a similar manner except that DNA encoding VEGF<sub>121</sub> (SEQ ID NO. 25), VEGF<sub>189</sub> (SEQ ID NO. 27) and VEGF<sub>206</sub> (SEQ ID NO.

28) is used in place of the VEGF<sub>165</sub>-encoding DNA in the above constructs, and. where necessary, appropriate amplification primers are selected.

VEGF-encoding DNA was obtained from plasmids designated pUC-121, pUC-165 and pUC-189 (the plasmids were the gift of Judith Abraham). Each of these plasmids had been prepared by inserting the respective DNA clone containing each form of VEGF linked to the signal peptide (see, SEQ ID NO. 26, nucleotides 13-90) into the BamHl site of the well known and commercially available vector pUC18 (for descriptions of this vector, see. e.g., U.S. Patent Nos. 5.114,840, 4.992.051.

4,968,613, 4,898,828; see, also Yanisch-Perron et al. (1985) Gene 33:103-119; Norrander et al. (1983) Gene 26:101-106; available from, for example, Life Technologies, Inc, Rockville, MD).

### 5 B. Construction of plasmids encoding VEGF-SAP fusion proteins

### 1. Construction of plasmids that contains DNA encoding VEGF165

#### a. Cloning

### (i) VEGF165-SAP constructs

The VEGF165-SAP constructs were prepared using the parental FGF:SAP vector pZ1B (pET 11a-based vector; see Example 2) that had been digested with NdeI and Ncol in order to remove the FGF-encoding portion of the DNA encoding the fusion protein, but leave the SAP-encoding portion intact. The FGF-encoding region was then replaced with the VEGF165-encoding DNA that has a NdeI site at the 5' end and a Ncol site at the 3' end.

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### (ii) VEGF165 constructs

To express the VEGF<sub>165</sub> protein without saporin, the pET11a vector was digested with *NdeI* and *BamHI* and the VEGF sequence inserted with the appropriate ends. For the constructs containing VEGF alone, the 3' primer contained a *BamHI* site for cloning and encodes a stop codon as follows:

5' GGATCCTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 64).

#### b. Amplification

#### (i) VEGF165-SAP constructs with the leader sequence

The constructs with the VEGF leader sequence were prepared from VEGF 165 as the template. For plasmids containing VEGF with the leader sequence or VEGF-SAP containing the leader sequence of the VEGF, the 5' primer contained a Ndel restriction enzyme site and encodes the signal sequence as follows:

- 5' CATATGAACTTTCTGCTGTCTTGG 3' (SEQ ID NO. 62), which contains a Ndel restriction enzyme site and encodes the signal. The Ncol site within VEGF165 was removed by SOE as the first step in the preparation of this construct using oligonucleotides of SEQ ID NOs. 60 and 61. The first round of PCR used oligos of SEQ ID NOs. 62 and 61 and SEQ ID NOs. 60 and 65.
- 5' TCCCAGGCTGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 60: sense primer); 5' TCCTCCTTCTGCCATTGGTGCAGCCTGGGA 3' (SEQ ID NO. 61: the complement or "antisense" primer); and 5' CCATGGCCGCCTCGGCTTGTC 3'(SEQ ID NO. 65: 3' primer that removes the stop codons and introduces a *Ncol* site).

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Amplification was performed as follows: denaturation for 1 min at 94°C annealing for 2 min at 70°C and extension for 2 min at 72°C for 35 cycles. Individual fragments were gel purified and subjected to a second round of amplification using only the external oligos (SEQ ID NOs. 62 and 65) under the same amplification conditions as above, to generate full length fragments which contain the appropriate cloning sites at the ends. After amplification and purification, the inserts are directionally cloned into the sites *Ndel/Ncol*-digested PZ1B.

## (ii) VEGF165-SAP constructs without the leader sequence

To prepare the constructs that lack DNA encoding the leader sequence, a similar amplification was performed with a primer similar to SEQ ID NO. 62, but lacking the signal sequence and beginning at position 1 of the mature protein as follows:

5' CATATGGCACCAATGGCAGAAGGAGGAGG 3'(SEQ ID NO. 63).

## 2. Construction of plasmids that contain DNA encoding VEGF121

The same type of constructs are generated using DNA encoding the VEGF121-encoding DNA, except that DNA encoding VEGF121 (see, SEQ. ID NO. 25) is used in place of the DNA encoding VEGF165. The initial step requires the mutagenesis of an internal *NcoI* site located at position 95 in the mature VEGF protein by nucleic acid amplification using the VEGF121-encoding DNA as a source of DNA.

The "sense" oligo the primer has the sequence:

5' TCCCAGGCTGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 60);
and the complement or "antisense" primer has the sequence:
5' TCCTCCTTCTGCCATTGGTGCAGCCTGGGA 3' (SEQ ID NO. 61) as described for VEGF165.

For the VEGF<sub>121</sub> or VEGF<sub>121</sub>-SAP constructs that contain the leader sequence the 5' primer has the following sequence:

5 'CATATGAACTTTCTGCTGTCTTGG 3' (SEQ ID NO. 62).

This primer contains a Ndel restriction enzyme site and encodes the signal sequence. A second amplification is performed with similar primer that lacks the signal sequence and begins at position 1 of the mature protein. This primer has the following sequence:

5' CATATGGCACCAATGGCAGAAGGAGGAGG 3' (SEQ ID NO. 63).

For the constructs containing VEGF alone, the 3' primer contains a BamHI site for cloning and encodes a stop codon. This primer has the following sequence:

#### 5' GGATCCTCATCACCGCCTCGGCTT 3'(SEQ ID NO. 64).

For the constructs designed to express the VEGF-SAP fusion protein, the stop codons have been removed and a *NcoI* site is introduced onto the 3' primer that has the sequence:

5' CCATGGCCGCCTCGGCTTGTC 3' (SEQ ID NO. 65).

The amplification conditions followed the above protocol.

### C. Construction of plasmids encoding SAP-VEGF fusion proteins

The following constructs have been prepared:

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- 1) SAP-VEGF<sub>121</sub>
- 2) SAP-VEGF<sub>165</sub>
- 3) SAP-linker-VEGF<sub>121</sub>
- 4) SAP-linker-VEGF<sub>165</sub>
- 5) SAP-linker-VEGF121-linker-VEGF121
- 6) SAP-linker-VEGF165-linker-VEGF165

in which the linker is (Gly4Ser)<sub>n</sub>, where n is selected from 1, 2 or 4. DNA encoding any other suitable peptide linker, see, e.g., SEQ ID NOs. 38-50, can be substituted for the exemplified linkers. For other constructs, see Table 3.

Constructs 1-4 serve as cloning intermediates for the final forms 5 and 6.

20 All forms have been completely characterized.

All cloning was performed using the vector pET-SAPMCS. The starting material for this vector can be PZIA or any of the pET 11a based vectors herein. Unmodified saporin can be cloned, using PCR amplification with appropriate primers, into the and Ncol sites of the pET11a-based vector. Using appropriate primers, an EcoRI site is added 5' to and adjacent to the NdeI site, and an EcoRI site is added 3' to 25 and adjacent to the Ncol site. The resulting amplified fragment is digested with EcoRI and subcloned into the EcoRl site of plasmid pGEM-4 (pGEM-4 serves as the source of the MCS, the pGEM series of plasmids are available from Promega, Madison WI; see also, U.S. Patent No. 4,766,072, which describes construction of the pGEM plasmids) in an orientation, such that the multicloning site (MCS) of pGEM-4 is 3' of the saporinencoding sequences. In such constructs, the resulting plasmid (pGEMSAP) was digested with PstI and the ends of the fragment were blunt-ended. The fragment was then digested with Ndel, thereby generating a fragment that contains all of the saporinencoding DNA and most of the MCS of pGEM-4. This fragment was then cloned into the Ndel/BamHI sites of pET 11a, in which the BamHI site had been blunt-ended by 35 filling in with Klenow polymerase and then cut with Ndel to produce Ndel/BamHl blunt ends. The resulting plasmid was designated PETSAP-MCS. It has unique Sacl.

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Smal, and Sall sites in the MCS for insertion of DNA encoding a desired linker, VEGF monomer, or combination of VEGF and linker 3' of the saporin-encoding DNA.

### 1. SAP-VEGF121 and SAP-VEGF165

The VEGF-encoding DNA is cloned downstream from SAP using the Ncol site at the C-terminus of SAP and one of several enzyme sites contained in the flanking region. For these constructs the VEGF molecule was amplified from cDNA using oligos that introduce a Ncol (CCATGG) site onto the N-terminus of the mature protein (and also remove an internal Ncol), and introduce a stop codon at the C-terminus of VEGF as well as a Sall (GTCGAC) site for cloning. In each case, the appropriate parental vector was digested with Ncol and Sall, and a Ncol/Sall digested insert was cloned into that site. PCR conditions were as for the amplification reactions described above.

Amplification was done using the following 5' sense oligo:

5' CCATGGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 51), and 3' anti-sense oligo:

5' GTCGACTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 52).

## 2. SAP-linker-VEGF121 and SAP-linker-VEGF165

For the generation of the linker-VEGF constructs, a different 5' primer that adds a NcoI site to the N-terminus, mutates the internal NcoI site and adds either the DNA encoding (Gly4Ser) (SEQ ID NO. 40), designated X1, or (Gly4Ser)2 designated X2 (SEQ ID NO. 41) onto the N-terminus of the VEGF molecule was used. The 3' primer was the above oligonucleotide (SEQ ID NO. 52). For the constructs with the (Gly4Ser)-encoding DNA, the 5' primer oligo was:

5' CCATGGGCGGCGGCTCTGCACCAATGGCAGAAGGA 3' (SEQ ID NO. 53).

For the (Gly2Ser)2 linker, this oligo was:

5'CCATGGGCGGCGGCTCTGGCGGCGGCGCTCTGCACCAATGGCAGAA GGA 3'

(SEQ ID NO. 54). The sequence of SAP-(Gly4Ser)- VEGF<sub>121</sub> is set forth in SEQ ID NO. 57. The sequence of SAP-(Gly4Ser)-VEGF<sub>165</sub> is set forth in SEQ ID NO. 58.

The construct in which the linker is (Gly4Ser)4 was prepared by digesting a plasmid (designated PZ74B or PZ74F) which contains SAP-AlaMet-VEGF165 construct with Ncol and inserting a fragment encoding Ncol- (Gly4Ser)4-Ncol (prepared, for example, by inserting codons encoding (Gly4Ser)2 between the Gly4Ser and Gly4Ser in SEQ ID NO. 41).

# 3. SAP-linker-VEGF165-linker-VEGF165 and SAP-linker-VEGF121-linker-VEGF121 constructs

For construction of the SAP-linker-VEGF-linker-VEGF constructs, the same 5'oligos were used for the constructs incorporating (Gly4Ser)<sub>1</sub> and (Gly4Ser)<sub>2</sub> (see, SEQ ID NOs. 53 and 54, respectively) and a set of 3' oligos were prepared that incorporated (Gly4Ser)<sub>1</sub> or (Gly4Ser)<sub>2</sub> and a NcoI site. The SAP-AlaMet-VEGF parental construct was digested with NcoI and the NcoI-linker-VEGF-NcoI fragment was inserted to produce constructs containing SAP-linker-VEGF-linker-VEGF.

The C-terminus oligos for the (Gly4Ser)<sub>1</sub> linker was:
5'CCATGGCAGAGCCGCCGCCGCCCCCCCCCTCGGCTTGTCACAT 3' (SEQ ID NO. 55). The (Gly4Ser)<sub>2</sub> linker for the 3' portion was (SEQ ID NO. 56):
5'CCATGGCAGAGCCGCCGCCGCCGCCCGCCTCGGCTTG TCACAT 3'. Amplification conditions were as described above.

The sequence of SAP-(Gly4Ser)-VEGF<sub>121</sub>-(Gly4Ser)-VEGF<sub>121</sub> is set forth is SEQ ID NO. 78 and the sequence of SAP-(Gly4Ser)-VEGF<sub>165</sub>-(Gly4Ser)-VEGF<sub>165</sub> is set forth in SEQ ID NO. 79.

## 4. SAP-Linker-VEGF121 constructs

These constructs were prepared in a similar manner to the VEGF165-containing constructs, except that plasmids containing VEGF121 were used as the starting materials.

## D. Expression of the SAP-VEGF and SAP-LINKER-VEGF constructs

The plasmids containing the various SAP-VEGF and SAP-LINKER-VEGF constructs (see Table 3) have been introduced into various vectors and host and are cultured under conditions suitable for expression in the selected host/vector. The resulting fusion protein is then purified as described for VEGF using heparin sulfate (see, e.g., U.S. Patent No. 5.219,739 to Tischer et al.; U.S. Patent No. 5.194,596 to Tisher et al.; U.S. Patent No. 5.240.848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications serial nos. 07/351.361. 07/369,424, 07/389,722. to Genentech, Inc., and any U.S. Patent based U.S. applications Serial Nos. 07/351.361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 A1 and EP 0 476 983 A1 to MERCK & CO.; Houck et al. (1991) Mol. Endo. 5:1806-1814). An affinity column with anti-SAP antibody may alternatively be used to purify VEGF conjugates, especially for SAP-VEGF121.

## E. Cytotoxicity of VEGF fusion protein conjugates

Cytotoxicity experiments are performed with the Promega (Madison. WI) CellTiter 96 Cell Proliferation/Cytotoxicity Assay. About 1,500 bovine or human aortic endothelial cells or other vascular endothelial cells are plated per well in a 96 well plate in 90 µl HDMEM plus 10% FCS and incubated overnight at 37°C, 5% CO2. The following morning 10 µl of media alone or 10 µl of media containing various concentrations of the fusion protein, VEGF dimer or saporin are added to the wells. The plate was incubated for 72°C hours at 37°C. Following the incubation period, the number of living cells are determined by measuring the incorporation and conversion of the commonly available dye MTT supplied as a part of the Promega kit. Fifteen µl of the MTT solution was added to each well, and incubation was continued for 4 hours. Next, 100 µl of the standard solubilization solution supplied as a part of the Promega kit are added to each well. The plate is allowed to stand overnight at room temperature and the absorbance at 560 nm was read on an ELISA plate reader (Titertek Multiskan PLUS, ICN, Flow, Costa Mesa, CA).

## EXAMPLE 5 BACULOVIRUS EXPRESSION OF VEGF

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#### A. Materials:

The VEGF constructs, including the VEGF121, VEGF121:SAP, VEGF165 and VEGF165:SAP constructs containing the leader sequences are introduced into a bacuolovirus vector pBluebac III (Invitrogen, San Diego, CA) and then co-transfected with wild type virus into insect cells Spodoptera frugiperda (sf9; see, e.g., Luckow et al. (1988) Bio/technology 6:47-55 and U.S. Patent No. 4,745,051) cells).

Antisera to VEGF was obtained from R&D/Peprotech (polyclonal antinative VEGF) and Santa Cruz (polyclonal anti-VEGF peptide antibody).

Constructs that are prepared include: VEGF<sub>121</sub> containing the leader sequence and VEGF<sub>165</sub> containing the leader sequence. The fusion proteins in which saporin is linked to the N-terminus of a VEGF monomer are presently preferred for baculovirus expression (and also bacterial expression). Heterologous leader sequences. discussed below, that direct secretion of the encoded fusion protein are added.

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#### B. Amplification

The template for these constructs is the VEGF121 or VEGF165 or the VEGF165:SAP construct containing the leader sequence in pET11a, described above. The 5' oligo (sense) for the VEGF121, VEGF121:SAP and VEGF165 constructs contains a *BamHI* I site for cloning into the vector and is as follows:

5' GGATCCGAAACATGAACTTTCTGCTGTCT 3' (SEQ ID NO. 66).

The VEGF<sub>165</sub>:SAP construct is amplified from the existing VEGF<sub>165</sub>:SAP insert in pET11a using the following 5' oligo, which contains a *BamHI* I site for cloning and is:

5' GGATCCGAAACATATGAACTTTCTGCTGTCT 3'(SEQ ID NO. 67). The 3' or non-coding oligo for the VEGF<sub>121</sub>:SAP or VEGF<sub>165</sub>:SAP constructs contains a *Pst*I I site for cloning into the vector and has the sequence: 5' CTGCAGGCCTCGTTTGACTACTT 3' (SEQ ID NO. 71).

The oligo for the 3' end of the VEGF<sub>121</sub> and VEGF<sub>165</sub> has the sequence (SEQ ID NO. 68): 3' CTGCAGTCATCACCGCCTCGGCTT 3'. Amplification follows the same protocol as described in the above Examples: denaturation for 1 min at 94°C, annealing for 2 min at 70°C, and extension for 2 min at 72°C for 35 cycles.

#### 20 C. Cloning

The inserts are directionally cloned into the BamHI/PstI sites of pBlueBac III.

## D. Preparation of VEGF molecules with an accessible cysteine residue at the N-terminus for chemical conjugation

VEGF molecules with an accessible cysteine residue at the N-terminus are constructed. These molecules can be chemically conjugated to one of the SAP muteins (Cys-1, +4 or +10 as described above). These constructs are as follows:

- 1) VEGF<sub>121</sub> with a cys at +4
- 2) VEGF<sub>165</sub> with a cys at +4
- 3) VEGF<sub>121</sub> with a cys at +2 followed by a Ncol site which makes this construct linker amenable.
- 4) VEGF165 with a cys at +2 followed by a NcoI site for the linker amenable form.

These constructs are designed such that the distance between the molecules (or accessible cysteines) can be increased by adding various linkers encoded on a Ncol (CCATGG) fragment, and thereby decrease any steric hindrance. The

presently preferred linkers are the linkers set forth in  $(Gly_4Ser)_n$ , in which n=1-4, linkers (see, SEQ ID NOs. 40 and 41, for n=1 and 2).

Amplification of the template for these constructs is VEGF<sub>121</sub> or VEGF<sub>165</sub>-encoding DNA (see, SEQ ID NOs. 25 and 26, respectively). The 5' sense oligo for the introduction/insertion of the mutations into the mature forms of the proteins VEGF<sub>121</sub>/165 cys+4 constructs (1 and (2 above) is: 5' TGGTCCCAGGCTGCACCCATGTGTGAAGGAGGAGGAGGAGAATCAT 3' (SEQ ID NO. 80).

The corresponding anti-sense mutational oligo is:

10 5' ATGATTCTGCCCTCCTTCACACATGGGTGCAGCCTGGGACCA 3'(SEQ ID NO. 81).

The 5' sense oligo for the introduction/insertion of the cys mutations into the mature forms of the proteins VEGF121/165 cys+2 Ncol constructs (3 and (4, above is:

15 5' GCCAAGTGGTCCCAGGCTGCATGTCCCATGGCAGAAGGAGGAGGGCAG 3' (SEQ ID NO. 82).

The corresponding anti-sense mutational oligo is:

- 5' CTGCCCTCCTTCTGCCATGGGACATGCAGCCTGGGACCACTTGGC 3' (SEQ ID NO. 83).
- The 5' sense oligo containing the *Bam*HI (GGATCC) cloning site for introduction into the baculovirus transfer vector pBlueBacIII for each of the above forms (1- (4, above. is:
  - 5' GGATCCGAAACATGAACTTTCTGCTGTCT 3' (SEQ ID NO. 66).

The 3' anti-sense oligo containing the *Pst*I (CTGCAG) site for cloning into the pBlueBacIII transfer vector for each of the above constructs is:

5' CTGCAGTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 68).

The constructs are prepared by splicing by overlap extension (SOE) by amplification of two pieces of the protein, which are then put together by the SOE technique. For example, to generate the VEGF cys+4 forms the first round of amplification uses oligos of SEQ ID NOs. 81 and 66 and SEQ ID NOs. 80 and 68. For the VEGF cys+2 Ncol constructs the first round of PCR would use oligos of SEQ ID NOs. 66 and 83 and 82 and 68. After amplification as follows: denaturation for 1 min at 94°C. annealing for 2 min at 70°C and extension for 2 min at 72°C. individual fragments are gel purified and subjected to a second round of amplification using only the external oligos (SEQ ID NOs. 66 and 68), under the same amplification conditions as above, to generate full length fragments which contain the appropriate cloning sites

at the ends. After amplification and purification, the inserts are directionally cloned into the *BamHI* and *PstI* sites of the pBlueBacIII transfer vector.

The constructs and corresponding Sequence Listing ID Nos. are as follows:

- 1) VEGF<sub>121</sub> cys +4 is set forth in SEQ ID NO. 86;
- 2) VEGF165 cys +4 is set forth in SEQ ID NO. 87;
- 3) VEGF<sub>121</sub> Cys+2 with Ncol sites is set forth in SEQ ID NO. 88;
  - 4) VEGF165 Cys+2 with NcoI is set forth in SEQ ID NO. 89.

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and

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## E. Preparation of SAP:VEGF constructs with heterologous signal (leader) sequences

Constructs containing a heterologous signal sequence in place of the VEGF signal sequence (see, e.g., amino acids 1-26 in SEQ ID NO. 33) or in addition to it are prepared. Such constructs are prepared using vectors such as pPBac and pMBac (available from Stratagene, San Diego, CA, see, also Lernhardt et al. (1993) Strategies 6:20-21), which contain the human alkaline phosphastase (see, e.g., Bailey et al. (1989) Proc. Natl. Acad. Sci. U. S. A. 86:22-26) and melittin (see, e.g., Tessier et al. (1991) Gene 98:177-183) secretory signals inserted into the BamHI and NdeI sites, respectively of pJVP10Z (see, e.g., Kawamoto et al. (1991) Biochem. Biophys. Res. Commun. 181:756-63, Ueda et al.(1994) Gene 140:267-272. Insertion of genes into the Smal/BamHI sites of these vectors results in fusion proteins that are directed into the insect cell secretory pathway, which processes the pro-polypeptide so that mature peptide or fusion protein is secreted into the growth medium.

Other heterologous signal sequences, such as the insulin signal sequence (see, e.g., U.S. Patent No. 4,431,746 for DNA encoding the signal sequence), the growth hormone signal sequence, mammalian alkaline phosphatase, the mellitin signal sequence and others that are processed by insect cells are used.

The heterologous signal sequences are used in other constructs as well.

30 including VEGF:SAP constructs, in order to direct the proteins encoded by operatively linked DNA into the periplasmic space or growth medium.

### F. Expression of the VEGF fusion protein-encoding constructs

The plasmids containing the various SAP-VEGF and SAP-linker-VEGF constructs (see Table 3) have been introduced into the baculovirus host and are cultured under conditions suitable for expression in the selected host/vector. The resulting fusion proteins are then purified.

## G. Characterization of the VEGF-SAP fusion protein

## Western blot of affinity-purified VEGF-SAP fusion protein

SDS gel electrophoresis was performed on a Phastsystem utilizing 10-15% gels (Pharmacia). Western blotting was accomplished by transfer of the electrophoresed protein to nitrocellulose using the PhastTransfer system (Pharmacia), as described by the manufacturer. The antisera to SAP and VEGF are used at a dilution of 1:1000 dilution. Horseradish peroxidase labeled anti-IgG was used as the second antibody (Davis et al. (1986) Basic Methods in Molecular Biology, New York, Elsevier Science Publishing Co., pp 1-338).

## 2. Assays to assess the cytotoxicity of the VEGF-SAP fusion protein

Effect of VEGF-SAP fusion protein on cell-free protein synthesis

The RIP activity of VEGF fusion protein is assayed as described in procedures for FGF conjugates (see, e.g., U.S. Patent No. 5,191,067).

## b. Cytotoxicity of VEGF-SAP fusion protein

Patent No. 5,191,067), except that vascular endothelial cells, such as a human or bovine aortic endothelial cells, are used. Prior to contacting with the VEGF conjugate the VEGF receptors can be up-regulated. Briefly, the cells are seeded at density of 1 - 5 x 10<sup>4</sup> cells/per well (in 24 well plates) and are incubated with varying concentrations of the test protein at 37°C for 5-7 days. Prior to contacting with the test protein the VEGF receptors can be upregulated, such as by replating or pretreating with VEGF. The cells are then trypsinized and counted in a Coulter counter.

# EXAMPLE 6 Expression of VEGF and VEGF-SAP in the PP $_{\text{L}}\text{-}\lambda$ system

The VEGF121, VEGF165. VEGF121:SAP. VEGF165:SAP. SAP:VEGF121, SAP:VEGF165 constructs are also expressed in the  $pP_L$ - $\lambda$  system (Pharmacia Fine Chemicals, see, also, U.S. Patent No. 5,227,469). This system is temperature inducible and directs the expressed protein to inclusion bodies thus protecting the protein from degradation. The EcoRI and XbaI sites are used for isolation of the VEGF or VEGF-SAP-encoding DNA from existing constructs.

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Constructs are cloned into the unique HpaI site of  $pP_L$ -lambda (see. e.g., Remaut et al. (1981) Gene 15:81, available from Pharmacia). The PL promoter, which is controlled by the cl repressor of  $\lambda$ , can be thermo-regulated using a bacterial host strain (N4830-1) containing the temperature-sensitive cl857 repressor. Induction is effected by raising the temperature.

All cloning is done in a host such as N99CI<sup>+</sup> and then transferred into N4830-1 for induction. Thus, the plasmid containing the construct is introduced into the host and grown at 30°C until A600 = 0.8-1.0. The temperature is raised to 42°C for 2 hours and the expressed protein is targeted to inclusion bodies.

For example, a plasmid, such as PZ70B1, is digested with Xbal/EcoR1 to release a fragment that contains the Xbal-ribosome binding site-VEGF165-SAP-T7 terminator-EcoR1 site, and the ends are filled in with Klenow reagent. Plasmid  $pP_L$ - $\lambda$  is digested with Hpal and the blunt-ended fragment is ligated into the digested plasmid. The plasmid is introduced into the N4830-1, grown at 30°C and induced at 42°C. The fusion protein is recovered from the inclusion bodies.

The inclusion bodies are released from the cells by concentrating the cells, such as by centrifugation, and are resuspended in a buffer (~0.4-0.6 M salt). The cells are lysed, either mechanically by homogenization or enzymatically, such as by treatment with lysozyme or EDTA. Soluble materials are removed by sequential centrifugation and resuspension or diafiltration. Further purification can be effected by centrifugation in a sucrose gradient.

The purified inclusion body fraction is then solubilized and the residual insoluble material is pelleted and discarded. Solubilization is effected using either guanidine HCl 100mM Tres, 150mM NaCl, 50mM EDTA and 50mM EGTA. Reducing agents, such as β-mercaptoethanol (0.1-0.3 M) and dithiothreitol (0.1 M) in the presence of EDTA are also used to disrupt disulfide bonds. The soluble protein fraction is recovered by centrifugation and diluted 10x into a buffer containing 100mM. This 10mM EDTA, 1% monothioglycerol and .25 M L-arginine, pH 9.5. The mixture is stored for 2 hours at 4°C and the centrifugation is repeated. Soluble protein is dialyzed in PBS to remove the monothioglycerol.

An acid phosphatase based assay is used to determine the level of proliferation induced by the addition of VEGF to human microvascular endothelial cells (HMVEC). Cells were seeded on Collagen I coated 96-well plates at  $2.5 \times 10^2$  cells/well in assay media. After overnight incubation, VEGF is added to each well in assay media. In general, concentrations from  $10^{-7}$  to  $10^{-12}$ M of each test compound is used. Cells are incubated for 3 days and fresh media containing the various VEGF compounds is added. Cells are assayed by a standard acid phosphatase assay on day 6.

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Protein synthesis inhibition is measured in a cell-free system. Samples are diluted in PBS, and 5 µl of diluted sample is added to 5 µl of reaction buffer containing 0.25 µg Brome mosaic virus RNA, 0.5 µl of a 1 mM amino acid mixture lacking leucine, 12.5 µCi <sup>3</sup>H leucine, and 15 µl of a nuclease-treated rabbit reticulocyte lysate. Samples are incubated for 1 hour at 30°C. The incubation is terminated by the addition of 375 µl of 1M NaOH in 2% H<sub>2</sub>O<sub>2</sub>. After 20 minutes, the volume is adjusted to 1.6 ml with H<sub>2</sub>O and 50 µl of the assay mixture, in duplicate, is transferred to a Multiscreen-HA 96 well filtration plate (Millipore, Bedford, MA, U.S.A.). Protein contents of each well were precipitated by adding 250 µl of ice-cold 30% trichloroacetic acid in 2% casamino acid. After incubation on ice for 30 min, TCA precipatable material was collected by washing the wells three times with 250 µl of ice cold 5% trichloroacetic acid. After drying, filter paper circles were punched out of the 96-well plate, inserted into vials containing 5 ml of BetaMax scintillation fluid (ICN, Costa Mesa, CA, U.S.A.) and counts were determined using a Beckman LS 6000SC liquid scintillation counter.

As shown in Figure 1, both VEGF<sub>121</sub> and VEGF<sub>165</sub> were produced in appreciable quantities at 2 hrs post-induction. Moreover dimerization occurred after refolding (Figure 2). VEGF<sub>121</sub> and VEGF<sub>165</sub> purified from inclusion bodies were able to induce proliferation of HMVEC cells as assayed by an acid phosphatase assay. HMVEC were grown for 72 hours in media lacking bFGF but which contained the test compounds in varying concentrations. On day 3 (72 hrs), an acid phosphatase assay was performed following standard procedures. Both the chemical conjugate of insect cell derived VEGF165 conjugated to SAP (CCSV) and SAP-VEGF121 (FPSV) produced from inclusion bodies in *E. coli* were able to inhibit the proliferation of HMVEC in a dose dependent manner at concentrations as low as 10-9M as compared to the level of stimulation seen with the addition of VEGF121 produced in insect cells. FPSV is a more potent inhibitor of cellular proliferation than CCSV. CCSV = chemical conjugate VEGF165-SAP; FPSV = SAP-VEGF121 made in *E. coli* from inclusion bodies; VEGF121 = insect cell derived; Saporin = SAP. (Figure 7)

Expression of VEGF<sub>121</sub>-SAP and VEGF<sub>165</sub>-SAP was also appreciable in the pP<sub>L</sub>- $\lambda$  system (Figure 4) and dimerized (Figure 5). In addition, VEGF<sub>121</sub> inhibited protein synthesis in a cell-free system indicating that SAP portion of the conjugate retained its ribosomal inactivating activity. (Figure 6)

## EXAMPLE 7 CHEMICAL SYNTHESIS OF VEGF-SAP AND SAP-VEGF

About 50-100 nmol of a VEGF, which is dialyzed against phosphatebuffered saline, is added to about 2.5 mg mono-derivatized SAP (a 1.5 molar excess over the VEGF protein) and left on a rocker platform overnight. The ultraviolet-visible wavelength spectrum is checked in order to determine the extent of reaction by the release of pyridylthione, which adsorbs at 343 nm with a known extinction coefficient. The reaction mixtures are treated for purification in the following manner: reaction 10 mixture is passed over a HiTrap heparin-Sepharose column (1 ml) equilibrated with 0.15 M sodium chloride in buffer A at a flow rate of 0.5 ml/min. The column is washed with 0.6 M NaCl and 1.0 M NaCl in buffer A and the product eluted with 4.0 M NaCl in buffer A. Fractions (0.5 ml) are analyzed by gel electrophoresis and absorbance at 280 nm. Peak tubes were pooled and dialyzed versus 10 mM sodium phosphate, pH 7.5 and applied to a Mono S 5/5 column equilibrated with the same buffer. A 10 ml gradient between 0 and 1.0 M sodium chloride in equilibration buffer are used to elute the product.

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#### **EXAMPLE 8**

## PREPARATION OF VEGF-SAP CONJUGATES THAT CONTAIN LINKERS ENCODING PROTEASE SUBSTRATES

#### Synthesis of oligos encoding protease substrates

- Complementary single-stranded oligos in which the sense strand encodes a protease substrate, have been synthesized either using a cyclone machine (Millipore) according the instructions provided by the manufacturer or, if greater than 80 bases, are made by Midland Certified Reagent Co. (Midland, TX). The following oligos have been synthesized and can be introduced into constructs encoding SAP: VEGF, VEGF: SAP as described above EXAMPLES 3 and 4.
  - Cathepsin B substrate linker:
  - 5'- CCATGGCCCTGGCCCTGGCCCTGCCATGG SEQ ID NO. 38
    - Cathepsin D substrate linker 2.
  - 5'- CCATGGGCCGATCGGGCTTCCTGGGCTTCCTGG GCTTCGCCATGG -3' SEQ ID NO. 39
    - Trypsin substrate linker
  - 5'- CCATGGGCCGATCGGGCGGTGGGTGCGCTGGTAATAGAGT

## CAGAAGATCAGTCGGAAGCAGCCTGTCTTGCGGTGGTCTC GACCTGCAGG CCATGG-3' SEQ ID NO. 44

- 4. Gly4Ser
- 5'- CCATGGGCGG CGGCGGCTCT GCCATGG -3' SEQ ID NO. 40
  - 5. (Gly4Ser)2
- 5'- CCATGGCGGCGCGCGCGCGCGCCTC TGCCATGG -3' SEQ ID NO. 41
  - 6. (Ser4Gly)4
- 10 CGTCGTCGGGCTCGTCGTCGGGCGCCATGG -3' SEQ ID NO. 42
  - 7. (Ser4Gly)2
  - - 8. Thrombin substrate linker
- 15 CTG GTG CCG CGC GGC AGC SEQ ID NO. 45

Leu Val Pro Arg Gly Ser

9. Enterokinase substrate linker GAC GAC GAC CCA SEQ ID NO. 46

Asp Asp Asp Lys

20 **10.** Factor Xa substrate ATC GAA GGT CGT SEQ ID NO. 47

lle Glu Gly Arg

11. Subtilisin linker

Xaa Ala His Tyr SEQ ID NO. 50, where Xaa is preferably Phe (see SEQ ID NO. 49).

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## B. Preparation of DNA constructs encoding SAP-Linker-VEGF

These constructs are prepared as described above for the SAP-(Gly4Ser)<sub>X</sub>-VEGF conjugates, except that DNA encoding the desired protease substrate is included in place of the DNA encoding (Gly4Ser)<sub>X</sub>.

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### **EXAMPLE 9**

### **CAM ASSAY FOR ANGIOGENESIS INHIBITION**

#### 35 Materials

Fertilized eggs are supplied by Melody Hill Ranch, Aptos, CA. L-[U<sup>14</sup>C] proline (specific activity, 290 mCi/mmole) is purchased from New England

Nuclear, Boston, MA. Type VII collgenase may be obtained from Sigma Chemical Co., St. Louis, MO. Silcone ring cups are obtained by cutting silicone tubing (3mm diameter) into small "O" rings of 1mm in thickness. These silicone ring cups can be reused many times if they are sterilized prior to each assay.

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### **Compound Preparation**

VEGF protein and peptide-based compounds are dissolved in water containing 0.5% methyl cellulose for testing. In general, 10  $\mu$ l of protein solution is implanted on each CAM.

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## Development of the CAM Assay for Angiogenesis Inhibition

The method of Folkman et al. (Developmental Biology 41:391-394, 1974) with minor modifications, is used to cultivate chicken embryos as follows:

Fresh fertile eggs are incubated for three days in a standard egg 15 incubator. On Day 3, eggs are cracked under sterile conditions and embryos are placed into 20 x 100mm plastic petri dishes and cultivated at 37°C in an embryo incubator with a water reservoir on the bottom shelf. Air is continuously bubbled into the water reservoir using a small pump such that the humidity in the incubator is kept constant. On Day 9, a sterile silicone ring cup is placed on each CAM and 0.25 uCi of <sup>14</sup>C-20 proline with or without the test materials dissolved in 0.5% methyl cellulose is delivered into each ring cup in a sterile hood. Ten embryos will be used in all control and test groups. After implantation of test materials, embryos are returned to the incubator and cultivation continued. On Day 12, all embryos are transferred into a cold room at 4-6°C. The antiangiogenic effect of each compound is first examined under the 25 microscope with 6x power followed by collagenase assay to give avascular zone scoring and <sup>14</sup>C-proline incorporation into collagenous protein respectively. embryos are kept on ice while scoring for avascular zone. Three color photographs will be taken of representative CAMs from each group that demonstrate significant positive responses.

## 30 Collagenase Assay for Measurement of <sup>14</sup>C-Proline Incorporation in Collagenous Protein

A piece of CAM 10mm in diameter is cut off under each ring cup and placed in a separate tube. 1.0mL of phosphate-buffered saline (PBS, pH 7.3) containing 0.11 and 0.17mg of cycloheximide and dipyridyl respectively is added. The tubes are placed in a boiling\_water bath for 10 minutes and then cooled to room temperature. The PBS in each tube is discarded after centrifugation at 3000 x g for 10 minutes. The CAM residue is washed once with 3mL of 15% TCA followed by 3 x

with 3mL of 5% TCA. Centrifugation is carried out as above between each washing. At this point, all non-protein bound radioactivity is removed and the CAM containing the newly synthesized <sup>14</sup>C-collagenous protein is suspended in 0.9mL of 0.1 NaOH and 1.1 mL of HEPES buffer at pH 7.4. The pH of the sample is neutralized with 0.8 N HCl using phenol red as indicator.

To digest the <sup>14</sup>C-collagenous protein, 7.5 units of collagenase and 500 nmoles of calcium chloride in 40 micro-liter of HEPES buffer is added to the above samples, and the mixtures are incubated at 37°C for 4 hours. The reaction is stopped by adding 1.0mL of 20% TCA containing 5mg of tannic acid into each tube. After vortexing, the samples are centrifuged at 3000 x g for 10 minutes. An aliquot of the clear supernatant is taken for scintillation counting to quantitate the radiolabeled tripeptides coresponding to basement membrane collagen and other collagenous materials synthesized by the CAM from <sup>14</sup>C-proline. The CAM pellets in each tube are solubilized in 0.5mL of 1.0 N NaOH by boiling in a water bath for 5 minutes. An aliquot of the dissolved CAM is used for protein determination using the method of Lowry (*J. Biol. Chem. 193:265-273*, 1951). The radioactivity per mg of protein from the CAM treated with a test compound relative to that from the control CAM gives the percent of inhibition.

Since modifications will be apparent to those of skill in this art, it is intended that this invention be limited only by the scope of the appended claims.

#### SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

(i) APPLICANT: Barbara A. Sosnowski

Kim Victor Lou Houston Michael Nova

- (ii) TITLE OF INVENTION: CONJUGATES OF VEGF WITH TARGETED AGENTS
- (iii) NUMBER OF SEQUENCES: 103
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Brown, Martin, Haller & McClain
  - (B) STREET: 1660 Union Street
  - (C) CITY: San Diego
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 92101-2926
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: Floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/213,446
  - (B) FILING DATE: 15-MAR-1994
  - (C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/213,447
  - (B) FILING DATE: 15-MAR-1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Seidman, Stephanie L.
  - (B) REGISTRATION NUMBER: 33,779
  - (C) REFERENCE/DOCKET NUMBER: 519522
  - (ix) TELECOMMUNICATION INFORMATION:
    - (A) TELEPHONE: (619)238-0999
    - (B) TELEFAX: (619)238-0062
- (2) INFORMATION FOR SEQ ID NO:1:
  - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_recomb
  - (B) LOCATION: 6..11
  - (D) OTHER INFORMATION: /standard\_name= "EcoRI Restriction Site"
- (ix) FEATURE:
  - (A) NAME/KEY: sig\_peptide
  - (B) LOCATION: 12..30
- (D) OTHER INFORMATION: /function= "N-terminal extension"

/product= "Native saporin signal peptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

## CTGCAGAATT CGCATGGATC CTGCTTCAAT

30

- (2) INFORMATION FOR SEQ ID NO:2:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: DNA (genomic)
  - (iv) ANTI-SENSE: YES
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_recomb
    - (B) LOCATION: 6..11
    - (D) OTHER INFORMATION: /standard\_name= "EcoRI Restriction Site"
  - (ix) FEATURE:
    - (A) NAME/KEY: terminator
    - (B) LOCATION: 23..25
    - (D) OTHER INFORMATION: /note= "Anti-sense stop codon"
  - (ix) FEATURE:
    - (A) NAME/KEY: mat\_peptide
    - (B) LOCATION: 26..30
    - (D) OTHER INFORMATION: /note= "Anti-sense to carboxyl terminus of mature peptide"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCAGAATT CGCCTCGTTT GACTACTTTG

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 804 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..804
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..804
  - (D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G4 in Example I.B.2."
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 46..804
  - (D) OTHER INFORMATION: /product= ""Saporin""
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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				TTA Leu										96
			GAT	AAA Lys				AAT				AAC		144
				GAC Asp			GTG				TCT			192
	CTT			AAT Asn		CAA				ACG				240
				AAC Asn 70					TAT				AAC	288
ACG	AAT	GTT	AAT	CGG	GCA	TAT	TAC	TTC	TCA	GAA	ATT	ACT	GCC	336

Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile Thr Ser Ala

85 90 GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT CAG AAA GCT Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala 105 TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT GCC CAG ATA Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile 432 120 ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu 480 135 CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys 528 150 155 AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA 576 Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Val 170 GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC 624 Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro Asn 180 185 AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg 672 195 200 AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT 720 Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn 210 215 AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 230 CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG 804 Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys

## (2) INFORMATION FOR SEQ ID NO:4:

245

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 804 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..804

(	ix	FEATURE:
---	----	----------

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..804
- (D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G1 in Example I.B.2."

#### (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
  (B) LOCATION: 46..804
- (D) OTHER INFORMATION: /product= "Saporin"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCA	TGG	ATC	CTG	CTT	CAA	TTT	TCA	GCT	TGG	ACA	ACA	ACT	GAT	GCG	GTC	48
Ala	Trp	Ile	Leu	Leu	Gln	Phe	Ser	Ala	Trp	Thr	Thr	Thr	Asp	Ala	Val	
-15					-10				_	- 5			-		1	
ACA	TÇA	ATC	ACA	TTA	GAT	CTA	GTA	AAT	CCG	ACC	GCG	GGT	CAA	TAC	TCA	96
Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	
			5					10				-	15	_		
TCT	TTT	GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	AAC	CTG	AAA	144
Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	
		20					25					30			_	
TAC	GGT	GGT	ACC	GAC	ATA	GCC	GTG	ATA	GGC	CCA	CCT	TCT	AAA	GAA	AAA	192
Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	-
	35					40					45					
TTC	CTT	AGA	ATT	AAT	TTC	CAA	AGT	TCC	CGA	GGA	ACG	GTC	TCA	CTT	GGC	240
Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	
50					55					60					65	
CTA	AAA	CGC	GAT	AAC	TTG	TAT	GTG	GTC	GCG	TAT	CTT	GCA	ATG	GAT	AAC	288
Leu	Lys	Arg	Asp		Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	
				70				٠	75					80		
																•
ACG	AAT	GTT	AAT	CGG	GCA	TAT	TAC	TTC	AGA	TCA	GAA	ATT	ACT	TCC	GCC	336
Inr	ASD	Val		Arg	Ala	Tyr	Tyr		Arg	Ser	Glu	Ile		Ser	Ala	
			85					90					95			
CNC		3.00														
		ACC														384
GIU	Den	Thr	ATA	Leu	Pne	PTO		Ala	Thr	Thr	Ala		Gln	Lys	Ala	
		100					105					110				
עידיים	CAA	TAC	מיאמ	CAA	מע עם		C 2 C	TCC	200	~~~			~~~	~-		
																432
neu	115	Tyr	1111	GIU	wab	120	GIN	Sei	TIE	GIU		Asn	AIA	GIN	IIe	
						120					125					
ACA	CAG	GGA	GAT	444	TCA	AGA	444	CAP	CTC	GGG	TTG	GGG	ATC	GAC	TTA	480
		Gly														460
130		7	-wp	~y =	135	Ar 9	-ya	314	nea	140	TE I	GIY	-1E		145	
										140					±43	-
لبطب	בידיים	ACG	TCC	ATC	GAA	GC Þ	CTC	244	שמע	מממ	GCA	ССТ	стс	تست	444	528

Ash Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Val 165 170 175  GCA CGA TTT CGG TAC ATT CAN ARC TTC GTD ARG TAG ARG TTC GTD ARG	Leu	Leu	Thr	Ser	Met 150	Glu	Ala	Val	Asn	Lys 155		Ala	Arg	Val	Val 160	Lys		
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro Asn 180  AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT 67: Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg 200  AAG ATT TCT ACG GCA ATA TAC GGA GAT GCC AAA AAC GGC GTG TTT AAT 720  Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn 215  AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG 768  Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 230  CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG  Sin Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	AAC Asn	GAA Glu	GCT Ala	Arg	TTT Phe	CTG Leu	CTT	ATC Ile	Ala	Ile	CAA Gln	ATG Met	ACA Thr	Ala	GAG Glu	GTA Val	5	76
Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg  195 200 205  AAG ATT TCT ACG GCA ATA TAC GGA GAT GCC AAA AAC GGC GTG TTT AAT  Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn  210 220 225  AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG  Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu  230 235 240  CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG  Sin Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	GCA Ala	CGA Arg	Phe	CGG Arg	TAC Tyr	ATT Ile	CAA Gln	Asn	TTG Leu	GTA Val	ACT Thr	AAG Lys	Asn	TTC Phe	CCC Pro	AAC Asn	63	24
Lys lie Ser Thr Ala ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn 220 225  AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 230 235 240  CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG 804	AAG Lys	Phe	GAC Asp	TCG Ser	GAT Asp	AAC Asn	Lys	GTG Val	ATT Ile	CAA Gln	TTT Phe	Glu	GTC Val	AGC Ser	TGG Trp	CGT Arg	61	72
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu 230 235 240  CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG  Sln Met Gly Leu Met Tyr Leu Gly Lys Pro Lys	Lys	ATT Ile	TCT Ser	ACG Thr	GCA Ala	Ile	TAC Tyr	GGA Gly	GAT Asp	GCC Ala	Lys	AAC Asn	GGC Gly	GTG Val	TTT Phe	Asn	72	20
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	aaa Lys	GAT Asp	TAT Tyr	GAT Asp	Phe	GGG Gly	TTT Phe	GGA Gly	AAA Lys	Val	AGG Arg	CAG Gln	GTG Val	Lys	Asp	TTG Leu	76	8
	CAA Gln	ATG Met	GGA Gly	Leu	CTT Leu	ATG Met	TAT Tyr	Leu	Gly	AAA Lys	CCA Pro	<b>AA</b> G Lys			. •		80	4

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 804 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..804
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1..804
  - (D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G2 in Example I.B.2."
- (ix) FEATURE:
  - (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 46..804
  - (D) OTHER INFORMATION: /product= "Saporin"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- GCA TGG ATC CTG CTT CAA TTT TCA GCT TGG ACA ACA ACT GAT GCG GTC

Ala -15	Trp	Ile	Leu	Leu	Gln -10	Phe	Ser	Ala	Trp	Thr -5	Thr	Thr	Asp	Ala	Val 1	
					GAT Asp											96
					ATC Ile											144
					ATA Ile										AAA Lys	192
					TTC Phe 55											240
					TTG Leu											288
					GCA Ala											336
					TTC Phe											384
					GAT Asp										ATA Ile	432
															TTA Leu 145	
CTT Leu	TTG Leu	ACG Thr	TTC Phe	ATG Met 150	GAA Glu	GCA Ala	GTG Val	AAC Asn	AAG Lys 155	AAG Lys	GCA Ala	CGT	GTG Val	GTT Val 160	AAA Lys	528
AAC Asn	GAA Glu	GCT Ala	AGG Arg 165	TTT	CTG Leu	CTT	ATC	GCT Ala 170	ATT	CAA Gln	ATG Met	ACA Thr	GCT Ala 175	Glu	GTA Val	576
			Arg		ATT			Leu					Phe		AAC Asn	624
AAG Lys	TTC Phe 195	Asp	TCG Ser	GAT Asp	AAC Asn	AAG Lys 200	Val	ATT	CAA Gln	TTT	GAA Glu 205	Val	AGC Ser	TGG Trp	CGT	672

	10	ie se	T ACG r Thr	AIA	215	Tyr	Gly	Asr	Ala	a Ly 22	s As	sn G	ly V	al F	he	<b>As</b> n 225		720
A)	AA GA Ys As	AT TA	T GAT	TTC Phe 230	GGG Gly	TTT Phe	GGA Gly	AAA Lys	GT( Val 235	L Ar	G CA g Gl	AG G' .n Va	TG A	ys A	AC sp 40	TTG Leu		768
G)	A AT in Me	G GGJ	Leu 245	CTT Leu	ATG Met	TAT Tyr	TTG Leu	GGC Gly 250	Lys	CC:	A AA o Ly	.G 's						804
(2	) IN	FORM	TION	FOR	SEQ	ID N	0:6:		•									
	(	(	QUENC A) LE B) TY C) ST D) TO	NGTH PE: : RAND:	: 80 nucl EDNE:	4 ba eic SS:	se p acid doub	air:	5									
	(i:	i) MO	LECUL	E TY	PE: 0	:DNA												
	(i	C	ATURE A) NA B) LO	ME/KI			04				-							
	(ix	(2	ATURE A) NAI B) LO	ME/KE	Υ: π N: 1	isc_ 80	feat	ture										
			) OTI	ier i	NFOR	MATI	ON:	/no	te= e cl	"Nuc	cleo M13	tide mpl	8-G	quen 7 in	ce Ex	amp]	le I.B	.2."
	(ix	(I :) FEJ (J (E		ER I COTY E/KE ATIO	NFOR espo Y: m N: 4	MATI ndin at_p 68	ON: g to	o th	e cl	one	M13	mp	18-G	quen 7 in	ce Ex	ampl	le I.B	.2."
		(I :) FEJ (J (E (I	TURE:	ER I COTT E/KE EATIO ER I	NFOR espo Y: m N: 4 NFOR	MATI ndin at_p 68 MATI	ON: epti 04 ON:	de /pro	e cl	one	M13	mp	18-G	quen	ce Ex	amp]	le I.B	.2."
GCA Ala -15	(xi	(I ) FEA (I (I ) SEQ	ATURE:	ER I COTT  E/RE CATIO ER I DES TT C. eu G.	NFOR espo Y: m N: 4 NFOR CRIP	MATI ndin at_p 68 MATI TION	epti 04 ON:	ide /pre	e cl oduc o No	:6:	M13	mp] orin	.# .#	in	Ex		le I.B	.2."
-15	(xi TGG Trp	(I (J (E (I ) SEC ATC Ile	ATURE: AT	ER I COTT  E/RE CATIO ER I DES TT C. eu G.	Y: m N: 4 NFOR CRIP AA T In Pl	MATI  at_p 68 MATI  TION  TT T he S	epti 04 ON: : SE CA G er A	ide /pro	e cl	t= " :6: ACA Thr -5	M13 Sape	mp] orin ACT Thr	GAT Asp	GCC Ala	Ex G' V	rc al 1	le I.B	
-15 ACA Thr	(xi TGG Trp TCA Ser	(I ) FEA (I ) SEC ATC Ile ATC Ile	ATURE: A) NAM B) LOC D) OTE CTG C Leu L ACA T Thr L	ER I COTT  E/RE CATIO ER I DES TT C. eu G.	Y: m N: 4 NFOR CRIP AA T In pl 10 AT C Sp Le	MATI ndin at_p 68 MATI TION TT T he S TA G SA A	epti 04 ON: : SE er A	ide /pro	e cl oduc NO TGG : Trp :	:6: ACA Thr -5 ACC Thr	M13 Sape ACA Thr GCG Ala	mp)  ACT Thr  GGT Gly	GAT Asp CAA Gln 15	GCC Ala TAC	Exc	TC al l CA er		48

TTC Phe 50	CTT Leu	AGA Arg	ATT	AAT Asn	TTC Phe 55	CAA Gln	AGT Ser	TCC Ser	CGA Arg	GGA Gly 60	ACG Thr	GTC Val	TCA Ser	CTT Leu	GGC Gly 65		240
CTA Leu	AAA Lys	CGC	GAT Asp	AAC Asn 70	TTG Leu	TAT Tyr	GTG Val	GTC Val	GCG Ala 75	TAT Tyr	CTT Leu	GCA Ala	ATG Met	GAT Asp 80	AAC Asn		288
ACG Thr	AAT Asn	GTT Val	AAT Asn 85	CGG Arg	GCA Ala	TAT Tyr	TAC	TTC Phe 90	AGA Arg	TCA Ser	GAA Glu	ATT Ile	ACT Thr 95	TCC Ser	GCC Ala		336
GAG Glu	TTA Leu	ACC Thr 100	GCC Ala	CTT Leu	TTC Phe	CCA Pro	GAG Glu 105	GCC Ala	ACA Thr	ACT	GCA Ala	AAT Asn 110	CAG Gln	AAA Lys	GCT Ala		384
TTA Leu	GAA Glu 115	TAC Tyr	ACA Thr	<b>GAA</b> Glu	GAT Asp	TAT Tyr 120	CAG Gln	TCG Ser	ATC Ile	GAA Glu	AAG Lys 125	AAT Asn	GCC Ala	CAG Gln	ATA Ile		432
ACA Thr 130	CAG Gln	GGA Gly	GAT Asp	AAA Lys	TCA Ser 135	AGA Arg	AAA Lys	GAA Glu	CTC Leu	GGG Gly 140	TTG Leu	GGG Gly	ATC Ile	GAC Asp	TTA Leu 145		480
CTT	TTG Leu	ACG Thr	TCC Ser	ATG Met 150	GAA Glu	GCA Ala	GTG Val	AAC Asn	AAG Lys 155	AAG Lys	GCA Ala	CGT Arg	GTG Val	GTT Val 160	AAA Lys		528
AAC Asn	GAA Glu	GCT Ala	AGA Arg 165	TTC Phe	CTT Leu	CTT	ATC Ile	GCT Ala 170	ATT Ile	CAG Gln	ATG Met	ACG Thr	GCT Ala 175	GAG Glu	GCA Ala		576
		TTT Phe 180														,	624
AAG Lys	TTC Phe 195	AAC Asn	TCG Ser	GAA Glu	AAC Asn	AAA Lys 200	GTG Val	ATT	CAG Gln	TTT Phe	GAG Glu 205	GTT Val	AAC Asn	TGG Trp	AAA Lys		672
_		TCT Ser	-	-	_											,	720
		TAT Tyr															768
		GGA Gly														;	804

- (2) INFORMATION FOR SEQ ID NO:7:
  - (i) SEQUENCE CHARACTERISTICS:

			(B) (C)	Leng Type Stra Topo:	: nu NDED	clei NESS	c ac : do	id uble								
	(i:	i) <b>M</b> (	OLEC	ULE :	TYPE	: cD	NA								٠	
	(i)			RE: NAME, LOCA:												
	(ix		(B) 1	NAME / LOCAT OTHER	NOI?	ORM	. 804 ATIO	V: /1	note:	= "Ni	icled Ml3	otide	≥ sed	nenc in	ce Example	e I.B.2
	(ix	··· (	B) I	RE: NAME/ JOCAT OTHER	'ION:	46.	.804			ict=	"Sap	orin	) <sup>#</sup>			
	(xi	) SE	QUEN	ICE D	ESCR	IPTI	ON:	SEQ	ID N	10 : 7 :			•			
GCA Ala -15	TGG	ATC	CTG Lev	CTT Leu	CAA Gln -10	Phe	TCA Ser	GCI Ala	Trp	ACA Thr	Thr	ACT Thr	GAT Asp	GCG Ala	GTC Val	4.6
ACA Thr	TCA Ser	ATC Ile	ACA Thr 5	TTA Leu	GAT Asp	CTA Leu	GTA Val	AAT Asn 10	Pro	ACC	GCG Ala	GGT Gly	CAA Gln 15	Tyr	TCA Ser	96
TCT Ser	TTT Phe	GTG Val 20	GAT Asp	AAA Lys	ATC Ile	CGA Arg	AAC Asn 25	AAC Asn	GTA Val	AAG Lys	GAT Asp	CCA Pro 30	AAC Asn	CTG Leu	AAA Lys	144
TAC Tyr	GGT Gly 35	GGT Gly	ACC Thr	GAC Asp	ATA Ile	GCC Ala 40	GTG Val	ATA Ile	GGC Gly	CCA Pro	CCT Pro 45	TCT Ser	AAA Lys	GAA Glu	AAA Lys	192
TTC Phe 50	CTT Leu	AGA Arg	ATT Ile	AAT Asn	TTC Phe 55	CAA Gln	AGT Ser	TCC Ser	CGA Arg	GGA Gly 60	ACG Thr	GTC Val	TCA Ser	CTT Leu	GGC Gly 65	240
CTA Leu	AAA Lys	CGC Arg	GAT Asp	AAC Asn 70	TTG Leu	TAT Tyr	GTG Val	GTC Val	GCG Ala 75	TAT Tyr	CTT Leu	GCA Ala	ATG Met	GAT Asp 80	AAC Asn	288
ACG Thr	AAT Asn	GTT Val	AAT Asn 85	CGG Arg	GCA Ala	TAT Tyr	TAC Tyr	TTC Phe 90	AGA Arg	TCA Ser	GAA Glu	ATT Ile	ACT Thr 95	TCC Ser	GCC Ala	336
GAG Glu	Leu	ACC Thr 100	GCC Ala	CTT Leu	TTC Phe	CCA Pro	GAG Glu 105	GCC Ala	ACA Thr	ACT Thr	GCA Ala	AAT Asn 110	CAG Gln	AAA Lys	GCT Ala	384

					GAT Asp											43	2
ACA Thr 130	CAA Gln	GGA Gly	gat Asp	CAA Gln	AGT Ser 135	AGA Arg	AAA Lys	GAA Glu	CTC Leu	GGG Gly 140	TTG Leu	GGG Gly	ATT	GAC Asp	TTA Leu 145	48	0
CTT Leu	TCA Ser	ACG Thr	TCC Ser	ATG Met 150	GAA Glu	GCA Ala	GTG Val	AAC Asn	AAG Lys 155	AAG Lys	GCA Ala	CGT Arg	GTG Val	GTT Val 160	AAA Lys	52	В
					CTT Leu											57(	6
					ATA Ile											624	4
					AAC Asn											672	2
					ATA Ile 215											720	O
					GGG											768	3
					ATG Met											804	4

#### (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_recomb
  - (B) LOCATION: 10..15
- (D) OTHER INFORMATION: /standard\_name= "Nco I restriction enzyme recognition site"
  - (ix) FEATURE:
    - (A) NAME/KEY: mat\_peptide

- (B) LOCATION: 15..22
- (D) OTHER INFORMATION: /product= "N-terminus of Saporin protein"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

#### CAACAACTGC CATGGTCACA TC

22

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 19 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
    - (ii) MOLECULE TYPE: DNA (genomic)
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_recomb
    - (B) LOCATION: 11..16
- (D) OTHER INFORMATION: /standard\_name= "Nco I restriction enzyme recognition site."
  - (ix) FEATURE:
    - (A) NAME/KEY: mat\_peptide
    - (B) LOCATION: 1..10
    - (D) OTHER INFORMATION: /product= "Carboxy terminus of mature FGF protein"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

## GCTAAGAGCG CCATGGAGA

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 21 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..12
    - (D) OTHER INFORMATION: /product= "Carboxy terminus of wild type FGF"
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_recomb
    - (B) LOCATION: 13..18
- (D) OTHER INFORMATION: /standard\_name= "Nco I restriction enzyme recognition site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCT AAG AGC TGACCATGGA GA Ala Lys Ser 1

21

- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 102 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..96
    - (D) OTHER INFORMATION: /product= "pFGFNcoI" /note= "Equals the plasmid pFC80 wih native FGF stop codon removed."
  - (ix) FEATURE:
    - (A) NAME/KEY: misc\_recomb
    - (B) LOCATION: 29..34
- (D) OTHER INFORMATION: /standard\_name= "Nco I restriction enzyme recognition site"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTT TTT CTT CCA ATG TCT GCT AAG AGC GCC ATG GAG ATC CGG CTG AAT
Leu Phe Leu Pro Met Ser Ala Lys Ser Ala Met Glu Ile Arg Leu Asn
1 5 10 15

GGT GCA GTT CTG TAC CGG TTT TCC TGT GCC GTC TTT CAG GAC TCC TGAAATCTT 102 Gly Ala Val Leu Tyr Arg Phe Ser Cys Ala Val Phe Gln Asp Ser 20 25 30

- (2) INFORMATION FOR SEQ ID NO:12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1230 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..1230
  - (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: /product= "bFGF"

### (ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 472..1230
- (D) OTHER INFORMATION: /product= "Saporin"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG Met	GCA Ala	GCA Ala	GGA Gly	TCA Ser 5	ATA Ile	ACA Thr	ACA Thr	TTA Leu	CCC Pro	GCC Ala	TTG Leu	CCC Pro	GAG Glu	GAT Asp	GGC Gly	48
GGC Gly	AGC Ser	GGC Gly	GCC Ala 20	TTC Phe	CCG Pro	CCC Pro	GGC Gly	CAC His	TTC Phe	AAG Lys	GAC Asp	CCC Pro	AAG Lys 30	CGG	CTG Leu	96
TAC Tyr	TGC Cys	AAA Lys 35	AAC Asn	GGG Gly	GGC Gly	TTC Phe	TTC Phe 40	CTG Leu	CGC <b>Ar</b> g	ATC Ile	CAC His	CCC Pro 45	GAC Asp	GGC Gly	CGA Arg	144
GTT Val	GAC Asp 50	GGG Gly	GTC Val	CGG Arg	GAG Glu	AAG Lys 55	AGC Ser	GAC Asp	CCT Pro	CAC His	ATC Ile 60	AAG Lys	CTT Leu	CAA Gln	CTT Leu	192
CAA Gln 65	GCA Ala	GAA Glu	GAG Glu	AGA Arg	GGA Gly 70	GTT Val	GTG Val	TCT Ser	ATC Ile	AAA Lys 75	GGA Gly	GTG Val	TGT Cys	GCT Ala	AAC Asn 80	240
CGT Arg	TAC Tyr	CTG Leu	GCT Ala	ATG Met 85	AAG Lys	GAA Glu	GAT Asp	GGA Gly	AGA Arg 90	TTA Leu	CTG Leu	GCT Ala	TCT Ser	AAA Lys 95	TGT Cys	288
GTT Val	ACG Thr	GAT Asp	GAG Glu 100	TGT Cys	TTC Phe	TTT Phe	TTT Phe	GAA Glu 105	CGA Arg	TTG Leu	GAA Glu	TCT Ser	AAT Asn 110	AAC Asn	TAC Tyr	336
		TAC Tyr 115														384
		GGG Gly														432
		CTT Leu														480
		TTA Leu														528

GT Va	G GA	T AA p Ly	A ATO	e Arg	AAA SAS	AAC Asr	GT/	A AA0 1 Ly:	s Ası	r cci	A AA D As:	C CT	G AA Ly 19	s Ty	C GGT	576
GG Gl	r ac	C GAG r As <sub>1</sub> 19!	b ITe	A GCC	GT(	ATA	GG( Gly 200	Pro	A CCT	TC1	r aai	A GAN S Glu 205	Ly:	A TT s Ph	C CTT e Leu	624
AG: Arg	A ATT	: ASI	r TTC	CAA Gln	AGT Ser	Ser 215	CGA Arg	GG#	ACC Thr	GTC Val	TCI Ser 220	Leu	GGC Gly	CT.	A AAA u Lys	672
CG( Arg 225	Asp	AAC Asr	TTG Leu	TAT Tyr	GTG Val 230	Val	GCG Ala	TAT Tyr	CTI	GCA Ala 235	Met	GAT Asp	AA( Asr	ACC Thi	AAT Asn 240	720
GTT Val	AAT	CGG Arg	GCA Ala	TAT Tyr 245	TAC	TTC Phe	AAA Lys	TCA Ser	GAA Glu 250	ATT	ACT Thr	TCC Ser	GCC	GA0	TTA Leu	768
ACC Thr	GCC	Leu	TTC Phe 260	Pro	GAG Glu	GCC Ala	ACA Thr	ACT Thr 265	GCA Ala	AAT Asn	CAG Gln	AAA Lys	GCT Ala 270	Leu	GAA Glu	816
TAC	ACA Thr	GAA Glu 275	Asp	TAT Tyr	CAG Gln	TCG Ser	ATC Ile 280	GAA Glu	AAG Lys	AAT Asn	GCC Ala	CAG Gln 285	ATA Ile	ACA Thr	CAG Gln	864
GGA Gly	GAT Asp 290	AAA Lys	AGT Ser	AGA Arg	AAA Lys	GAA Glu 295	CTC Leu	GGG Gly	TTG Leu	GGG Gly	ATC Ile 300	GAC Asp	TTA Leu	CTT	TTG Leu	912
ACG Thr 305	TTC Phe	ATG Met	GAA Glu	GCA Ala	GTG Val 310	AAC Asn	AAG Lys	AAG Lys	GCA Ala	CGT Arg 315	GTG Val	GTT Val	AAA Lys	AAC Asn	GAA Glu 320	960
GCT Ala	AGG Arg	TTT Phe	CTG Leu	CTT Leu 325	ATC Ile	GCT Ala	ATT Ile	CAA Gln	ATG Met 330	ACA Thr	GCT Ala	GAG Glu	GTA Val	GCA Ala 335	CGA Arg	1008
TTT Phe	AGG Arg	TAC	ATT Ile 340	CAA Gln	AAC Asn	TTG Leu	GTA Val	ACT Thr 345	AAG Lys	AAC Asn	TTC Phe	CCC Pro	AAC Asn 350	<b>AA</b> G Lys	TTC Phe	1056
GAC Asp	TCG Ser	GAT Asp 355	AAC Asn	AAG Lys	GTG Val	ATT Ile	CAA Gln 360	TTT Phe	GAA Glu	GTC Val	AGC Ser	TGG Trp 365	CGT Arg	AAG Lys	ATT Ile	1104
TCT Ser	ACG Thr 370	GCA Ala	ATA Ile	TAC Tyr	Gly	GAT ( Asp /	GCC Ala	AAA Lys	AAC Asn	Gly	GTG Val 380	TTT Phe	AAT Asn	AAA Lys	GAT Asp	1152
TAT Tyr 385	GAT Asp	TTC Phe	GGG Gly	Phe	GGA . Gly :	AAA ( Lys '	GTG . Val .	AGG Arg	Gln '	GTG : Val :	AAG Lys	GAC Asp	TTG Leu	CAA Gln	ATG Met 400	1200

						G GG											1230
GI	y Det	·	u Me	40		u Gl	у Гу	s Pr	0 Ly 41								
/21	TRI	ZODW:	3 T T ()	T BO													
(2)	INI	·ORM	ATTO	N FO	R SE	Q ID	NO:	13:									
	<b>(</b> )					ACTE											
		1	(A) I	LENG:	TH: :	1230	base	pa:	irs								
						cleid											
						TESS:											
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	(ii	.) MC	LECT	TLE	TYPE:	cDN	IA										
	(ix		ATU														
						CDS											
		(	B) I	.OCAI	: NOI	1	1230	)									
	(ix	-	ATUR														
		(	A) N	IAME/	KEY:	mat	_pep	tide								-	•
						1									-		
		(	D) C	THER	INF	ORMA	TION	: /p	rodu	ct=	"bFG	F"					
	(ix	) FE	ATUR	E:													
		(	A) N	AME/	KEY:	mat	_pep	tide									
						472											
		(	D) O	THER	INF	ORMA	TION	: /p	rodu	ct=	"Sap	orin	**		•		
														÷	,		
	(xi	) SE	QUEN	CE D	ESCR	IPTI	ON:	SEQ	ID N	0:13	:						
ATG	GCT	GCT	GGT	TCT	ATC	ACT	ACT	CTG	CCG	GCT	CTG	cce	GA A	GAC	GGT		48
Met	Ala	Ala	Gly	Ser	Ile	Thr	Thr	Leu	Pro	Ala	Leu	Pro	Glu	Asp	Gly		40
1				5					10					15	02,		
GGT	TCT	GGT	GCT	TTC	CCG	ccc	GGC	CAC	<u>т</u> тС	AAG	GAC	ccc	AAG	ccc	CTG		96
Gly	Ser	Gly	Ala	Phe	Pro	Pro	Glv	His	Phe	Lve	Aen	Pro	Live	720	Lau		90
_		•	20					25		-,-	p		30	~-9	<b>2</b> -0		
TR (	maa																
TAC	TGC	AAA	AAC	GGG	GGC	TTC	TTC	CTG	CGC	ATC	CAC	CCC	GAC	GGC	CGA		144
ıyı	Сув					Phe								Gly	Arg		
		35					40					45					
STT	GAC	GGG	GTC	CGG	GAG	AAG	AGC	GAC	CCT	CAC	ATC	AAG	CTT	CAA	CTT		192
Val		Gly	Val	Arg	Glu	Lys	Ser	Asp	Pro	His	Ile	Lys	Leu	Gln	Leu		
	50					55					60						
CAA	GCA	GAA	GAG	AGA	GGA	GTT	GTG	TCT	ATC	AAA	GGA	GTG	TGT	GCT	AAC		240
3ln	Ala	Glu	Glu	Arg	Gly	Val	Val	Ser	Ile	Lys	Gly	Val	Cys	Ala	Asn		
65					70					75	-		-		80		
CGT	TAC	CTG	GCT	ATC	AAG	GAA	ሞፈጋ	GGA	DGD.	עידיי	Carc	تحس	ساس	תתת	ستاس		200
Arq	Tyr	Leu	Ala	Met	Lve	Glu	Aen	Glv	727	LAN	LIG	7] =	201	Tare	Che		288
_	- 4 -			R5	-,, 5		~3p	U2 y	MIG	<b>₽</b>	T-C II	A14	261	Dys	-ya		

					TTC Phe												336
					AGG Arg												384
	Thr	GGG			AAA Lys	Leu	GGA				Gly	CCT					432
					CCA											-	480
145	Ile	Leu	Phe	Leu	Pro 150	Met	Ser	Ala	Lys	Ser 155	Ala	Met	Val	Thr	<b>Ser</b>		
					GTA Val												528
					AAC Asn		Val										576
					GTG Val												624
					AGT Ser												672
					GTG Val 230												720
					TAC Tyr												768
					GAG Glu												816
					CAG Gln												864
					AAA Lys												912
ACG Thr	TTC Phe	ATG Met	GAA Glu	GCA Ala	GTG Val	AAC Asn	AAG Lys	AAG Lys	GCA Ala	CGT Arg	GTG Val	GTT Val	AAA Lys	AAC Asn	GAA Glu		960

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305					310					315					320	
GCT Ala	AGG Arg	TTT Phe	CTG Leu	CTT Leu 325	ATC Ile	GCT Ala	ATT	CAA Gln	ATG Met 330	ACA Thr	GCT Ala	GAG Glu	GTA Val	GCA Ala 335	CGA Arg	1008
TTT Phe	AGG Arg	TAC Tyr	ATT Ile 340	CAA Gln	AAC Asn	TTG Leu	GTA Val	ACT Thr 345	AAG Lys	AAC Asn	TTC Phe	CCC Pro	AAC Asn 350	AAG Lys	TTC Phe	1056
GAC Asp	TCG Ser	GAT Asp 355	AAC Asn	AAG Lys	GTG Val	ATT Ile	CAA Gln 360	TTT Phe	GAA Glu	GTC Val	AGC Ser	TGG Trp 365	CGT Arg	AAG Lys	ATT Ile	1104
TCT Ser	ACG Thr 370	GCA Ala	ATA Ile	TAC Tyr	GGG Gly	GAT Asp 375	GCC Ala	AAA Lys	AAC Asn	GGC Gly	GTG Val 380	TTT Phe	AAT Asn	AAA Lys	GAT Asp	1152
TAT Tyr 385	GAT Asp	TTC Phe	GGG Gly	TTT Phe	GGA Gly 390	AAA Lys	GTG Val	AGG Arg	CAG Gln	GTG Val 395	AAG Lys	GAC Asp	TTG Leu	CAA Gln	ATG Met 400	1200
		CTT														1230
(2)		(E	UENC	E CH NGTH PE: RANI	IARAC I: 59 nucl		STIC e pa acid sing	S: irs						-		
	(ii)	MOL	ECUL	E TY	PE:	DNA	(gen	omic	:)		٠					
	(ix)	FEA (D			INFO	RMAT	'ION :	/pr	oduc	t= t	rp p	romo	ter			
	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:14:						
AATI	cccc	TG T	TGAC	AATI	TA A	CATC	GAAC	TAG	TTAA	CTA	GTAC	GCAG	CT T	GGCT	GCAG	59
(2)	INFO	RMAT	ION	FOR	SEQ	ID N	0:15	i:								
	(i)	(B	) LE ) TY ) ST	ngth PE : RAND	: 59 nucl EDNE	TERI bas eic SS: line	e pa acid sing	irs								

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

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(D) OTHER INFORMATION/product= bacteriophage lambda cII : binding site	ribosome
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GTCGACCAAG CTTGGGCATA CATTCAATCA ATTGTTATCT AAGGAAATAC TTACATATG	59
(2) INFORMATION FOR SEQ ID NO:16	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 66 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 166     (D) OTHER INFORMATION: /product= VEGF gene EXON I (VEGF)</pre>	LEADER
SEQUENCE -265)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16	
ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC TTG CTC Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu  1 10 15	48
TAC CTC CAC CAT GCC AAG Tyr Leu His His Ala Lys	66
20 (2) INFORMATION FOR SEQ ID NO:17	•
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 52 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	·
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 152     (D) OTHER INFORMATION: /product= VEGF gene EXON II</pre>	· .
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17	
TGG TCC CAG GCT GCA CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His 1 5 10 15	48
GAA G Glu	52

(2) INFORMATION FOR SEQ ID NO:18	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 197 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 3197     (D) OTHER INFORMATION: /product= VEGF gene EXON III</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18	
TG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile  1 5 10 15	47
GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr 20 25 30	95
ATC TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys 35 40 45	143
AAT GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr 50 55 60	191
ATG CAG Met Gln 64	197
(2) INFORMATION FOR SEQ ID NO:19	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 77 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 175     (D) OTHER INFORMATION: /product= VEGF gene EXON IV</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19	
ATT ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC	48

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120

Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser 110 115 TTC CTA CAG CAC AAC AAA TGT GAA TGC AG 77 Phe Leu Gln His Asn Lys Cys Glu Cys 130 135 140 (2) INFORMATION FOR SEQ ID NO:20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both (ii) MOLECULE TYPE: genomic (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..27 (D) OTHER INFORMATION: /product= VEGF gene EXON V (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20 A CCA AAG AAA GAT AGA GCA AGA CAA GAA AA 30 Pro Lys Lys Asp Arg Ala Arg Gln Glu 5 (2) INFORMATION FOR SEQ ID NO:21 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 72 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both (ii) MOLECULE TYPE: genomic (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 2..70 (D) OTHER INFORMATION: /product= VEGF gene EXON VI (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21 A AAA TCA GTT CGA GGA AAG GGA AAG GGG CAA AAA CGA AAG CGC AAG AAA Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys 1 TCC CGG TAT AAG TCC TGG AGC GT 72 Ser Arg Tyr Lys Ser Trp Ser 20

(2) INFORMATION FOR SEQ ID NO:22

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(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 51 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 151     (D) OTHER INFORMATION: /product= Insert between EXON VI &amp; V</pre>	II
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22	
TAC GTT GGT GCC CGC TGC TGT CTA ATG CCC TGG AGC CTC CCT GGC CCC Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp Ser Leu Pro Gly Pro  1 5 10 15	48
CAT His	51
(2) INFORMATION FOR SEQ ID NO:23	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 132 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: double  (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: genomic	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 2130     (D) OTHER INFORMATION: /product= EXON VII  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23</pre>	
T CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT Pro.Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp 1 5 10 15	49
CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys 20 25 30	97
GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AG Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys 35 40	.32
(2) INFORMATION FOR SEQ ID NO:24	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 22 base pairs

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		(0	) S7	TRAN	nuc DEDN DGY :	ESS:	dou									
	(ii)	MOL	ECUI	LE T	YPE:	gen	omic									
	(xi)	(B	) NZ	ME/I	KEY: ION: INFO	2:		: /p:	rodu	ct= :	EXON	VII	ı			
	(xi)	SEQ	UENC	E DI	ESCR:	[PTI	ON: 8	SEQ :	ID N	0:24						
		AC AA Sp Ly					<b>SA</b>									22
(2)	INFO	RMAT	ION	FOR	SEQ	ID I	10:2	5	•							
	(i)	(B (C	) LE ) TY ) SI	ngti Pe : Rani	HARA( H: 4° NUC) DEDNI DGY:	73 ba Leic ESS:	ase p acid doul	pair:	<b>5</b>							 
-	(ii)	MOL	ECUI	E TY	PE:	cDN3	4									
	(ix)	(B	) NA	ME/F	ŒY: ION: INFO	13		: /g/	rodu	ct= '	"VEGI		-ence	oding	j DNA	
		(B (D	) NA ) LC ) OT	ME/F CATI THER		13.	MOIT				leade	er-ei	ncod:	ing (	seque	nce
		SEQ								_	-					
GGA.	rccga	VAA C				_	_		_		_	is T		GC CT		46
		CTG Leu 15														96
		GAA Glu														144
		TAT Tyr														.192
														•		

ATC Ile	TTC Phe	CAG Gln	GAG Glu	TAC Tyr 65	CCT Pro	GAT Asp	GAG Glu	ATC Ile	Glu	TAC Tyr	ATC Ile	TTC Phe	AAG Lys	Pro	TCC Ser	2	240
TGT	GTG	ccc	CTG	ATG	CGA	TGC	GGG	GGC	70 TGC	TGC	TAA	GAC	GAG	75 GGC	CTG	2	. 8 8
Сув	Val	Pro	Leu B0	Met	Arg	Сув	Gly	Gly 85	Cys	Cys	Asn	Asp	Glu 90	Gly	Leu		
GAG Glu	TGT Cys	GTG Val	CCC Pro	ACT Thr	GAG Glu	GAG Glu	TCC Ser	AAC Asn	ATC Ile	ACC Thr	ATG Met	CAG Gln	ATT Ile	ATG Met	CGG Arg	3	36
		95_	-				100					105			-		
Ile	Lys 110	Pro	His	Gln	Gly	CAG Gln 115	His	Ile	GGA Gly	GAG Glu	Met 120	AGC Ser	TTC	CTA Leu	CAG Gln	3	84
CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	aga	CAA	GAA	4	32
125	ASD	Lys	Сув	Glu	Cys 130	Arg	Pro	Lys	Lys	<b>Asp</b> 135	Arg	Ala	Arg	Gln	Glu 140		
			AAG Lys			CGG Arg	TGAT	rgaa?	A ADT	TGAG	GATO	C.				4	73
(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10:26	;:			٠						
	(i)	SEC	ITENC	E CH	APAC	י מינידי	CTT/	·c .									

- (1) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 605 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 13..588
  - (D) OTHER INFORMATION: /product= "VEGF165-encoding DNA"
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 13..90
  - (D) OTHER INFORMATION: /product= "leader sequence-encoding DNA".
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:
- GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT

  Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu

  1 5 10
- GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC 96
  Ala Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro

		15					20					25				
ATG Met	GCA Ala 30	GAA Glu	GGA Gly	GGA Gly	GGG Gly	CAG Gln 35	AAT Asn	CAT	CAC His	GAA Glu	GTG Val 40	GTG Val	AAG Lys	TTC Phe	ATG Met	144
GAT Asp 45	GTC Val	TAT Tyr	CAG Gln	CGC Arg	AGC Ser 50	TAC Tyr	TGC Cys	CAT His	CCA Pro	ATC Ile 55	GAG Glu	ACC	CTG Leu	GTG Val	GAC Asp 60	192
ATC Ile	TTC Phe	CAG Gln	GAG Glu	TAC Tyr 65	CCT Pro	GAT Asp	<b>GA</b> G Glu	ATC Ile	GAG Glu 70	TAC Tyr	ATC Ile	TTC Phe	AAG Lys	CCA Pro 75	TCC Ser	240
TGT Cys	GTG Val	CCC Pro	CTG Leu 80	ATG Met	CGA Arg	TGC Cys	GGG Gly	GGC Gly 85	TGC Cys	TGC Cys	AAT Asn	GAC Asp	GAG Glu 90	GGC Gly	CTG Leu	288
GAG Glu	TGT Cys	GTG Val 95	CCC Pro	ACT Thr	GAG Glu	Glu	TCC Ser 100	AAC Asn	ATC Ile	ACC Thr	ATG Met	CAG Gln 105	ATT	ATG Met	CGG Arg	336
ATC Ile	AAA Lys 110	CCT Pro	CAC His	CAA Gln	GGC	CAG Gln 115	CAC His	ATA Ile	GGA Gly	GAG Glu	ATG Met 120	AGC Ser	TTC Phe	CTA Leu	CAG Gln	384
CAC His 125	AAC Asn	AAA Lys	TGT Cys	GAA Glu	TGC Cys 130	AGA Arg	CCA Pro	AAG Lys	AAA Lys	GAT Asp 135	AGA Arg	GCA Ala	AGA Arg	CAA Gln	GAA Glu 140	432
AAT Asn	CCC Pro	TGT Cys	GGG Gly	CCT Pro 145	TGC Cys	TCA Ser	GAG Glu	CGG Arg	AGA Arg 150	AAG Lys	CAT His	TTG Leu	TTT Phe	GTA Val 155	CAA Gln	480
GAT Asp	CCG Pro	CAG Gln	ACG Thr 160	TGT Cys	AAA Lys	TGT Cys	TCC Ser	TGC Cys 165	AAA Lys	AAC Asn	ACA Thr	GAC Asp	TCG Ser 170	CGT Arg	TGC Cys	528
AAG Lys	GCG Ala	AGG Arg 175	CAG Gln	CTT Leu	GAG Glu	TTA Leu	AAC Asn 180	GAA Glu	CGT Arg	ACT Thr	TGC Cys	AGA Arg 185	TGT Cys	GAC Asp	AAG Lys	576
Pro	AGG Arg	CGG Arg	TGAT	GAA1	GA A	TGAG	GATO	:c								605

## (2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 677 base pairs
  - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: double
    - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

	(i:	x) F														
				NAME												
				LOCA'												
			(D) (	OTHE	R IN	FORM	ATIO	N: /	prod	uct=	"VE	GF <sub>18</sub>	9- <b>e</b> n	codi	ng DNA"	
	(i:	k) Fl	EATU	RE:												
				NAME,	/KEY	: CD	s									
				LOCA:												
								V: /1	produ	ıct=	"lea	ader	sem	Jence	e-encodin	מזגרו היי
																ig DAA
	(xi	L) SI	EQUE	NCE I	DESC	RIPT:	ION:	SEQ	ID 1	10:27	7					
GGI	TCCC		~~ ,									•				
GG	***	MAA		ATG A	AC I	TT (	TIG (	TIG 7	CT 1	rgg d	TG (	AT 1	rgg ,	AGC (	TT	4
				Met &	usn e	ne i	Jeu I	.eu s	er 1	tp /	al F	lis 7		er I	en	
				•				•					10			
GCC	TTG	CTG	CTO	TAC	CTC	CAC	CAT	GCC	· AAC	TGG	: דר <u>י</u> ר	CAC	:		CCC	
Ala	Leu	Leu	Leu	Tyr	Leu	His	His	Ala	Lys	TI	Ser	Gln	Ala	Ala	Pro	96
		15	i				20	)	•			25				
ATG	GCA	GAA	GGA	GGA	GGG	CAG	AAT	CAT	CAC	GAA	GTG	GTG	AAG	TTC	ATG	144
met	30 A18	GIU	GLY	Gly	Gly			His	His	Glu	Val	Val	Lys	Phe	Met	
	30					35	1				40					
GAT	GTC	TAT	CAG	CGC	AGC	TAC	TGC	СУТ	CCN	אתר	CNC		ama.		GAC	
Asp	Val	Tyr	Gln	Arq	Ser	Tvr	Cvs	His	Pro	Tle	GAG	かわっ	Lau	GTG	Asp	192
45		_		_	50	- 2 -	-3-			55	GIU	****	Deu	VAI	<b>AS</b> P	
ATC	TTC	CAG	GAG	TAC	CCT	GAT	GAG	ATC	GAG	TAC	ATC	TTC	AAG	CCA	TCC	240
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	
				65					70					75		
TGT	GTG	CCC	CTG	ATG	CGA	TCC	CCC		<b>m</b> 00							
Cys	Val	Pro	Leu	Met	Ara	CVE	GIV	GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	288
•			80			Cys	Gry	85	cys	Cys	ASI	Asp	90	GIA	Leu	
GAG	TGT	GTG	CCC	ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	336
Glu	Сув	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	
		95					100					105				
ATC	444	CCT	CNC	CAA	~~~	~~~										
Ile	Lvs	Pro	Hie	CAA Gln	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	384
	110		••••	<b>G</b> 211	Gry	115	пть	TIE	GIY	GIU	120	Ser	Pne	Leu	GIn	
											120					
CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	AAG	AAG	GAT	AGA	GCA	AGA	CAA	GAA	432
His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	
125					130					135					140	
מממ	222	TCN														
Lvs	LVE	Ser	U-1	CGA	GGA	AAG	GGA	AAG	GGG	CAA	AAA	CGA	AAG	CGC	AAG	480
-,-	-15		val	Arg 145	Grà	Lys	GIA	гÀг	150	GIN	гÀг	Arg	тàг		Lys	
						•			130					155	•••	
AAA	TCC	CGG	TAT	AAG	TCC	TGG	AGC	GTT	CCC	TGT	GGG	CCT	TGC	TCA	GAG	528
Lys	Ser	Arg	Tyr	Lys	Ser	Trp	Ser	Val	Pro	Cys	Gly	Pro	Cys	Ser	Glu	•

			160					165					170			
CGG Arg	AGA Arg	AAG Lys 175	CAT His	TTG Leu	TTT Phe	GTA Val	CAA Gln 180	GAT Asp	CCG Pro	CAG Gln	ACG Thr	TGT Cys 185	AAA Lys	TGT Cys	TCC Ser	576
TGC Cys	AAA Lys 190	AAC Asn	ACA Thr	gac Asp	TCG Ser	CGT Arg 195	TGC Cys	AAG Lys	GCG Ala	AGG Arg	CAG Gln 200	CTT Leu	GAG Glu	TTA Leu	AAC Asn	624
GAA Glu 205	CGT Arg	ACT Thr	TGC Cys	AGA Arg	TGT Cys 210	GAC Asp	AAG Lys	CCG Pro	AGG Arg	CGG Arg 215	TGA	rgaa'	rga i	ATGA(	GGATCC	677
(2)	(ii) (ix)	SEC () () () () () MOI () () () () () () ()	QUENCAL LECUI	CE C	HARACI: 72 nucl DEDNI DEDNI DETNI DE	CDS 13	STIC ise pacid doub 711 TION:	CS: Dairs i ole	coduc						DNA"	o DNA
	(xi)	SEC											•			_
GGAT	rccg#	AA C										s Tr		C CI		48
														GCA Ala		96
														TTC Phe		144
														GTG Val		192
_														CCA Pro 75		240

161	GIG		CIG	ATG	CGA	TGC	GGG	GGC	TGC	TGC	TAA :	GAC	GAG	GGC	CTG	288
Cys	Val	Pro	Leu 80	Met	Arg	Cys	Gly	Gly 85	Cys	Cys	Asn	Asp	Glu 90		Leu	
GAG	TGT	GTG	ccc	ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	336
Glu	Cys	Val 95	Pro	Thr	Glu	Glu	Ser 100		Ile	Thr	Met	Gln 105		Met	Arg	
ATC	AAA	CCT	CAC	CAA	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	384
Ile	Lys 110	Pro	His	Gln	Gly	Gln 115	His	Ile	Gly	Glu	Met 120	Ser	Phe	Leu	Gln	
CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	AAG	AAG	GAT	AGA	GCA	AGA	CAA	GAA	432
125	ASD	Lys	Cys	Glu	Сув 130	Arg	Pro	Lys	Lys	<b>As</b> p 135	Arg	Ala	Arg	Gln	Glu 1 <b>4</b> 0	
AAA	AAA	TCA	GTT	CGA	GGA	AAG	GGA	AAG	GGG	CAA	AAA	CGA	AAG	CGC	AAG	480
Lys	Lys	Ser	Val	Arg 145	Gly	Lys	Gly	Lys	Gly 150		Lys	Arg	Lys	Arg 155	Lys	
AAA	TCC	CGG	TAT	AAG	TCC	TGG	AGC	GTT	TAC	GTT	GGT	GCC	CGC	TGC	TGT	528
Lys	ser	Arg	191 160	Lys	Ser	Trp	Ser	Val 165	Tyr	Val	Gly	Ala	Arg 170	Cys	Cys	
CTA	ATG	ccc	TGG	AGC	CTC	CCT	GGC	CCC	CAT	ccc	TGT	GGG	CCT	TGC	TCA	576
Leu	Met	Pro 175	Trp	Ser	Leu	Pro	Gly 180	Pro	His	Pro	Cys	Gly 185	Pro	Сув	Ser	
GAG	CGG	AGA	AAG	CAT	TTG	TTT	GTA	CAA	GAT	CCG	CAG	ACG	TGT	AAA	TGT	624
iIU	190	Arg	Lys	His	Leu	Phe 195	Val	Gln	Asp	Pro	Gln 200	Thr	Cys	Lys	Cys	
rcc	TGC	AAA	AAC	ACA	GAC	TCG	CGT	TGC	AAG	GCG	AGG	CAG	CTT	GAG	TTA	672
Ser 205	Cys	Lys	Asn	Thr	<b>Asp</b> 210	Ser	Arg	Сув	Lys	Ala 215	Arg	Gln	Leu	Glu	<b>Leu</b> 220	
AAC	GAA	CGT	ACT	TGC	AGA	TGT	GAC	AAG	CCG	AGG	CGG	TGAT	GAAT	'GA		718
Asn 225	Glu	Arg	Thr	Сув	Arg 230	Cys	Asp	Lys	Pro	<b>Arg</b> 235	Arg					
<b>ATGA</b>	GGAT	.cc														728

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 768 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 4..768

		(1	D) O	THER	INF	ORMA	TION	: /p	rodu	ct=	"SAP	CYS	+4"			
	(ix	()		AME/												
				OCAT: THER				: /p:	rodu	ct=	"mat	ure	SAP	CYS	+4"	•
	(xi	SE	QUEN	CE D	escr:	IPTI(	ON: 3	SEQ	ID N	0:29	:					
CAT	ATG	GTC	ACA	TCA	TGT	ACA	TTA	GAT	CTA	GTA	AAT	CCG	ACC	GCG	GGT	41
	1	AGI	1111	sei	<b>5</b>	THE	ren	Asp	ren	10	Asn	Pro	Thr	Ala	Gly 15	
CAA	TAC	TCA	TCT	TTT	GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	96
Gln	Tyr	Ser	Ser	Phe 20	Val	Asp	Lys	Ile	Arg 25	Asn	Asn	Val	Lys	qaA 0 E	Pro	
AAC	CTG	AAA	TAC	GGT	GGT	ACC	GAC	ATA	GCC	GTG	ATA	GGC	CCA	CCT	TCT	144
Asn	Leu	Lys	Tyr 35	Gly	Gly	Thr	Asp	Ile 40	Ala	Val	Ile	Gly	Pro	Pro	Ser	7,1
AAA	445	AAA	רדים	لملم	<b>V</b> CV	ינייני ע	אמע		CAA	n CT	TCC	CCD		ACG	CTC.	100
Lys	Glu	Lys 50	Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	192
							55	_				60				
	Leu													CTT Leu		240
	65					70					75					
ATG Met	GAT Asp	AAC Asn	ACG Thr	AAT Asn	GTT Val	AAT Asn	CGG Arg	GCA Ala	TAT	TAC	TTC Phe	AAA Lys	TCA Ser	GAA Glu	ATT Ile	288
80					85					90		-			95	
														GCA Ala		336
				100		,			105	<b>51</b> u	A. a		****	110	<b>75</b> 11	
														AAG		384
3111	rys	ATA	115	GIU	TYT	Thr	GIU	120	TYT	GIn	ser	11e	125	Lys	Asn	
														TTG		432
Ala	Gln	Ile 130	Thr	Gln	Gly	Asp	Lys 135	Ser	Arg	Lys	Glu	Leu 140	Gly	Leu	Gly	
														GCA		480
Ile	Asp 145	Leu	Leu	Leu	Thr	Phe 150	Met	Glu	Ala	Val	Asn 155	Lys	Lys	Ala	Arg	
GTG	GTT	AAA	AAC	GAA	GCT		Trifit	CTG	СТТ	ATC		ATT	CAA	ATG	ACA	528
Val					Ala					Ile				Met	Thr	
160					165					170					175	

GC	T GA	G GT	A GCA	CGA	TIT	AGG	TAC	ATT	CAA	AAC	TTG	GTA	ACT	AAG	AAC	57
Al	a Gl	u Val	Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Thr	Lys	Asn	
				180					185					190		
TT	C CC	CAAC	AAG	TTC	GAC	TCG	GAT	AAC	AAG	GTG	ATT	CAA	لملتك	CDA	GTC	. 62
Ph	e Pr	Asn	Lys	Phe	Asp	Ser	Asp	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	. 62
			195					200					205			
AG	C TG	GCGT	' AAG	АТТ	T)	D.C.C.	GCN	እ <b>ሞ</b> እ	T > C	000	<b>~~</b>					
Se	r Trj	Arg	Lys	Ile	Ser	Thr	Ala	Ile	TVT	GGG	Asp	GCC Ala	AAA Luce	AAC	GGC	67:
		210					215		- 3 -	01,	, wp	220	Lys	ASII	GIY	
<b></b>	~ ~~															٠.
Va	l Phe	TAA T	Lve	GAT	TAT	GAT	TTC	GGG	TTT	GGA	AAA	GTG	AGG	CAG	GTG	720
-	225	Asn	Lyo	жър	ıyı	230	Pne	GIY	Phe	Gly	Lys 235	Val	Arg	Gln	Val	
AA	GAC	TTG	CAA	ATG	GGA	CTC	CIT	ATG	TAT	TTG	GGC	AAA	CCA	AAG	TAG	768
240	a wab	Leu	Gln	Met	Gly 245	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys		
					445					250					255	
	•															
(2)	INF	ORMA:	TION	FOR	SEQ	ID N	0:30	:								
	(i	) SE(	TIPNO	יים ריים	ממגי	T d'an	CPT C									
	` -		A) LE													
		(E	3) TY	PE:	nucl	eic.	acid	all 5								
			C) ST													
		(1	) TO	POLO	GY: :	both										
	(ii	) MOL	ECUL	E TY	PE:	CDNA									-	
	(1X	) FEA	LTURE L) NAI	-	E32	-										
			) LO				S.R									
			) OT					/pro	oduc	t= "!	SAP (	TYS -	+10"			
								•								
	(1X)	FEA			<b></b>											
			) NAI							•						
			) OTI					/pro	duct	C= "N	natur	e SZ	4P (~	/S ±1		
								•		•						
	( <b>v</b> i)	CEO.	TENO													
	(*1)	SEQ	DENCE	e DES	CRIF	LION	i: SE	Q II	NO:	:30:						
CAT	ATG	GTC 2	ACA 1	CA A	ATC A	CA I	TA G	AT C	TA C	TA T	יפד כ	ירה זי	יככ פ	ירה מ	CT.	48
	Met	Val '	Thr S	er 1	le 1	hr L	eu A	sp L	eu 1	al c	ys F	ro I	hr A	la G	ily	40
	1				5					10	-				15	
CAA	TAC	<b>ጥ</b> ሮኔ '	<b>~~~~~~~</b>	- 10 day	*****	· > 47 -	nn -	mc -								
Gln	Tyr	TCA :	Ser F	he v	al A	SD I	MA A	le A	GA A	AC A	LAC G	TA A	AG G	AT C	CA	96
	-		_	20	**		·, - •		25		V		ys M	.sp	10	
AAC	CTG	AAA :	TAC G	GT G	GT A	CC G	AC A	TA G	CC G	TG A	TA G	GC C	CA C	CT I	CT	144

Asn	Leu	Lys	Tyr 35	Gly	Gly	Thr	Asp	Ile 40	Ala	Val	Ile	Gly	Pro 45	Pro	Ser	
				CTT Leu												192
				AAA Lys												240
				AAT Asn											ATT Ile 95	288
				TTA Leu 100												336
				GAA Glu												384
				CAG Gln												432
				TTG Leu												480
	Val			GAA Glu												528
				CGA Arg 180												576
		_	-	TTC Phe												624
				ATT Ile												672
				GAT Asp												720
	Asp			ATG Met											TAG 255	768

(2	INFORMATION	FOR	SEQ	ID	NO:31:	:
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12/ DECUMENCE CHARACTERISTICS	(i)	SEQUENCE	CHARACTERISTICS
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- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: CDNA

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1212
- (D) OTHER INFORMATION: /product= "VEGF121-SAP LEADER pZ1B"

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..81
- (D) OTHER INFORMATION: /product= "LEADER"

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAT	ATG Met 1	AAC Asn	TTT	CTG Leu	CTG Leu 5	Ser	TGG	GTG Val	CAT His	TGG Trp 10	Ser	CTT	GCC	TTG Leu	CTG Leu 15	48
CTC Leu	TAC Tyr	CTC Leu	CAC His	CAT His 20	GCC Ala	AAG Lys	TGG	TCC	CAG Gln 25	GCT Ala	GCA Ala	CCA Pro	ATG Met	GCA Ala 30	GAA Glu	96
GGA Gly	GGA Gly	GGG Gly	CAG Gln 35	AAT Asn	CAT His	CAC His	GAA Glu	GTG Val 40	GTG Val	AAG Lys	TTC Phe	ATG Met	GAT Asp 45	GTC Val	TAT Tyr	144
CAG Gln	CGC Arg	AGC Ser 50	TAC Tyr	TGC Cys	CAT His	CCA Pro	ATC Ile 55	GAG Glu	ACC Thr	CTG Leu	GTG Val	GAC Asp 60	ATC Ile	TTC Phe	CAG Gln	192
GAG Glu	TAC Tyr 65	CCT Pro	GAT Asp	GAG Glu	ATC Ile	GAG Glu 70	TAC Tyr	ATC Ile	TTC Phe	AAG Lys	CCA Pro 75	TCC Ser	TGT Cys	GTG Val	CCC Pro	240
CTG Leu 80	ATG Met	CGA Arg	TGC Cys	GGG Gly	GGC Gly 85	TGC Cys	TGC Cys	AAT Asn	GAC <b>As</b> p	GAG Glu 90	GGC Gly	CTG Leu	GAG Glu	TGT Cys	GTG Val 95	288
CCC Pro	ACT Thr	GAG Glu	GAG Glu	TCC Ser 100	AAC Asn	ATC Ile	ACC Thr	ATG Met	CAG Gln 105	ATT Ile	ATG Met	CGG Arg	ATC Ile	AAA Lys 110	CCT Pro	336
														AAC Asn		384

115 120 125 TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAA TGT GAC 432 Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp 130 135 AAG CCG AGG CGG CCA TGG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT 480 Lys Pro Arg Arg Pro Trp Val Thr Ser Ile Thr Leu Asp Leu Val Asn 145 150 CCG ACC GCG GGT CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC 528 Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn GTA AAG GAT CCA AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA 576 Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile 180 GGC CCA CCT TCT AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC 624 Gly Pro Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser 195 200 CGA GGA ACG GTC TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC 672 Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val 210 GCG TAT CTT GCA ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC 720 Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe 225 AAA TCA GAA ATT ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC 768 Lys Ser Glu Ile Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala 245 250 ACA ACT GCA AAT CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG 816 Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser 265 ATC GAA AAG AAT GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA 864 Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu 280 CTC GGG TTG GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC 912 Leu Gly Leu Gly Ile Asp Leu Leu Thr Phe Met Glu Ala Val Asn 295 AAG AAG GCA CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT 960 Lys Lys Ala Arq Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala 310 ATT CAA ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG 1008 Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu 325 330 GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT 1056

133

Va	1 Th	r Ly	's As	n Phe 340	Pro	Asn	Lys	Phe	34	p Se 5	r As	p As	n L		/al		
CA Gl	A TT n Ph	T GA e Gl	A GT u Va 35	C AGC l Ser	TGG	CGT Arg	AAG Lys	Ile 360	e Se	T AC	G GC	A AI a Il	A Ti e Ty 36	/T G	GG ly	GAT Asp	110
GC: Al:	C AAI a Lys	A AA S As: 37	n GT	GTG Val	TTT Phe	AAT Asn	AAA Lys 375	Asp	TA:	r ga r As	T TT p Ph	C GG e Gl 38	y Pi	T G	GA ly	AAA Lys	115
GT(	3 AG0 1 Arg 385	GI	G GTG	AAG Lys	GAC Asp	TTG Leu 390	CAA Gln	ATG Met	GG# Gly	CT(	C CT Let 39	u Me	G TA t Ty	T T	TG eu	GGC Gly	1200
	Pro		S TAG	•						- •	-						1212
(2)	INF	ORM	TION	FOR	SEQ	ID N	10:32	2 :									
	(ii	( ( ( ) MO ) FE ()	ATURIAN LA	AME/K	I: 12 nucl DEDNE GY: TPE: CY: ( ON: 4	eic ss: both cDNA	ase acid both	pai:		it= '	"VEG	F165	- SAI	, <b>n</b> o	Li	EADER	
	(xi)	SE	QUENC	E DE	SCRII	PTIO	1: S	EQ I	D NO	):32	:						
CAT	ATG Met 1	GCA Ala	CCA Pro	ATG (	GCA ( Ala (	GAA ( Glu (	GGA (	GGA Gly	GGG Gly	CAG Gln 10	AAT Asn	CAT His	CAC	GA:	A G	STG /al 15	48
STG Val	AAG Lys	TTC Phe	ATG Met	GAT ( Asp \ 20	GTC 1	TAT C	CAG (	CGC . Arg .	AGC Ser 25	TAC Tyr	TGC Cys	CAT His	CCA Pro	ATO	<b>G</b>	AG Slu	96
CC Thr	CTG Leu	GTG Val	GAC Asp 35	ATC :	rrc c Phe G	AG G	SAG 1	rac ( Fyr 1	CCT Pro	GAT Asp	GAG Glu	ATC Ile	GAG Glu 45	TAC	: A	TC le	144
TC he	AAG Lys	CCA Pro 50	TCC Ser	TGT (	GTG C	cc c	TG A	ATG (	CGA Arg	TGC Cys	GGG Gly	GGC Gly 60	TGC Cys	TGC	A	AT sn	192

GAC Asp	GAG Glu 65	GGC Gly	CTG Leu	GAG Glu	TGT Cys	GTG Val 70	CCC Pro	ACT Thr	GAG Glu	GAG Glu	TCC Ser 75	AAC Asn	ATC	ACC Thr	ATG Met		240
CAG Gln 80	ATT	ATG Met	CGG Arg	ATC Ile	AAA Lys 85	CCT	CAC His	CAA Gln	GGC Gly	CAG Gln 90	CAC His	ATA Ile	GGA Gly	GAG Glu	ATG Met 95		288
Ser	Phe	CTA Leu	Gln	His 100	Asn	Lys	Суѕ	Glu	Cys 105	Arg	Pro	Lys	Lys	<b>As</b> p	Arg		336
Ala	Arg	CAA Gln	Glu 115	Asn	Pro	Cys	Gly	Pro 120	Cys	Ser	Glu	Arg	Arg 125	Lys	His	•	384
Leu	Phe	Val 130	Gln	Asp	Pro	Gln	Thr 135	Cys	Lys	Cys	Ser	Cys 140	Lys	Asn			432
Asp	Ser 145	CGT Arg	Cys	Lys	Ala	Arg 150	Gln	Leu	Glu	Leu	<b>As</b> n 155	Glu	Arg	Thr	Cys		480
Arg	Суѕ	GAC Asp	Lys	Pro	Arg 165	Arg	Pro	Trp	Val	Thr 170	Ser	Ile	Thr	Leu	<b>As</b> p 175		528
Leu	Val	AAT	Pro	Thr 180	Ala	Gly	Gln	Tyr	Ser 185	Ser	Phe	Val	Asp	Lys 190	Ile		576
Arg	Asn	AAC	Val 195	Lys	Asp	Pro	Asn	<b>Leu</b> 200	Lys	Tyr	Gly	Gly	Thr 205	Asp	Ile		624
Ala	Val	ATA Ile 210	Gly	Pro	Pro	Ser	Lys 215	Glu	Lys	Phe	Leu	<b>Arg</b> 220	Ile	Asn	Phe		672
Gln	<b>Ser</b> 225	TCC Ser	Arg	Gly,	Thr	Val 230	Ser	Leu	Gly	Leu	Lys 235	Arg	Asp	Asn	Leu		720
Tyr 240	Val	GTC Val	Ala	Tyr	<b>Leu</b> 245	Ala	Met	Asp	Asn	Thr 250	Asn	Val	Asn	Arg	Ala 255		768
Tyr	Tyr	TTC Phe	Lys	<b>Ser</b> 260	Glu	Ile	Thr	Ser	Ala 265	Glu	Leu	Thr	Ala	Leu 270	Phe	·	816
		GCC Ala					Gln										B64

AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA ATG Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Leu Thr Phe Met Glu 315  GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG Ala Val Asn Lys Lys Ala Arg Val Val Lys Asn Glu Ala Arg Phe Leu 320  CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile 340  CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC GIN Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn 365  AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile 370  TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TYR Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 385  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400  TAT TTG GGC AAA CCA AAG TAG		TAT	CAG Gln	TCG Ser 290	ATC Ile	GAA Glu	AAG Lys	AAT Asn	GCC Ala 295	CAG Gln	ATA Ile	ACA Thr	CAG Gln	GGA Gly 300	GAT Asp	AAA Lys	AGT Ser	912
Ala Val Asn Lys Lys Ala Arg Val Val Lys Asn Glu Ala Arg Phe Leu 320 335  CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile 340 345 350  CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn 365  AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile 370 375  TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TYT Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 390  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400  TAT TTG GGC AAA CCA AAG TAG TAG TAG TYT Leu Gly Lys Pro Lys 420		AGA Arg	Lys	GAA Glu	CTC Leu	GGG Gly	TTG Leu	Gly	ATC Ile	GAC Asp	TTA Leu	CTT Leu	Leu	Thr	TTC Phe	ATG Met	GAA Glu	960
Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile 350  CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn 365  AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile 370  TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TYr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 385  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400  TAT TTG GGC AAA CCA AAG TAG TYr Leu Gly Lys Pro Lys 420		Ala	Val	AAC Asn	AAG Lys	AAG Lys	Ala	CGT Arg	GTG Val	GTT Val	AAA Lys	Asn	GAA Glu	GCT Ala	AGG Arg	TTT Phe	Leu	1008
Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn 365  AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile 370  TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 385  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Met 405  TAT TTG GGC AAA CCA AAG TAG TAG TYr Leu Gly Lys Pro Lys 420		CTT Leu	ATC Ile	GCT Ala	ATT Ile	Gln	ATG Met	ACA Thr	GCT Ala	GAG Glu	Val	GCA Ala	CGA Arg	TTT Phe	AGG Arg	Tyr	ATT Ile	1056
Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile 370 375 380  TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 385 390 395  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400 405 410 415  TAT TTG GGC AAA CCA AAG TAG TYR Leu Gly Lys Pro Lys 420					Val					Pro					Ser			1104
Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly 385  TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400  TAT TTG GGC AAA CCA AAG TAG Tyr Leu Gly Lys Pro Lys 420	•		Val	Ile					Ser					Ser				 1152
Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met 400 405 410 415  TAT TTG GGC AAA CCA AAG TAG Tyr Leu Gly Lys Pro Lys 420			Gly					Gly					Asp					 1200
Tyr Leu Gly Lys Pro Lys 420		Phe					Gln					Gln					Met	1248
(2) INFORMATION FOR SEQ ID NO:33:		Tyr	Leu	Gly	Lys	Pro 420	Lys		10:33	:								1269

#### . . .

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1369 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

#### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..1352
- (D) OTHER INFORMATION: /product= "VEGF165-SAP LEADER BAC"

### (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..89

# (D) OTHER INFORMATION: /product= "LEADER"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala											50			
					CAC His									98
					CAG Gln 35									146
					TAC Tyr									194
					gat Asp				Tyr					242
					TGC Cys									290
					GAG Glu					Met				338
					CAG Gln 115									386
					AGA Arg									434
					TCA Ser									482
					TGT Cys						-			530
					TTA Leu									578
					ACA Thr									626

190	)				195	;				200					205	
GCG Ala	GG1 Gly	CAA Gln	TAC	Ser 210	Ser	TTT Phe	GTG Val	GAT Asp	Lys 215	Ile	CGA Arg	AAC Asn	AAC Asn	GT# Val 220	AAG Lys	674
GAT Asp	Pro	AAC Asn	CTG Leu 225	Lys	TAC	GGT Gly	GGT	Thr 230	Asp	: ATA	GCC Ala	GTG Val	ATA Ile 235	Gly	CCA Pro	722
CCT	TCT Ser	Lys 240	Glu	AAA Lys	TTC Phe	CTT Leu	AGA Arg 245	Ile	AAT Asn	TTC Phe	CAA Gln	AGT Ser 250	Ser	CGA Arg	GGA Gly	770
ACG Thr	GTC Val 255	Ser	CTT	GGC	CTA Leu	AAA Lys 260	CGC Arg	GAT Asp	AAC Asn	TTG Leu	TAT Tyr 265	GTG Val	GTC Val	GCG	TAT	818
CTT Leu 270	GCA Ala	ATG Met	GAT Asp	AAC Asn	ACG Thr 275	AAT Asn	GTT Val	AAT Asn	CGG Arg	GCA Ala 280	TAT	TAC Tyr	TTC Phe	AAA Lys	TCA Ser 285	<b>866</b> 
GAA Glu	ATT	ACT	TCC	GCC Ala 290	GAG Glu	TTA Leu	ACC Thr	GCC Ala	CTT Leu 295	TTC Phe	CCA Pro	GAG Glu	GCC Ala	ACA Thr 300	ACT	914
GCA Ala	AAT Asn	CAG Gln	AAA Lys 305	GCT Ala	TTA Leu	GAA Glu	TAC Tyr	ACA Thr 310	GAA Glu	GAT Asp	TAT Tyr	CAG Gln	TCG Ser 315	ATC Ile	GAA Glu	962
AAG Lys	AAT Asn	GCC Ala 320	CAG Gln	ATA Ile	ACA Thr	CAG Gln	GGA Gly 325	GAT Asp	AAA Lys	AGT Ser	AGA Arg	AAA Lys 330	GAA Glu	CTC Leu	GGG Gly	1010
TTG Leu	GGG Gly 335	ATC Ile	GAC Asp	TTA Leu	CTT Leu	TTG Leu 340	ACG Thr	TTC Phe	ATG Met	GAA Glu	GCA Ala 345	GTG Val	AAC Asn	AAG Lys	AAG Lys	1058
GCA Ala 350	CGT Arg	GTG Val	GTT Val	AAA Lys	AAC Asn 355	GAA Glu	GCT Ala	AGG Arg	TTT Phe	CTG Leu 360	CTT Leu	ATC Ile	GCT Ala	ATT Ile	CAA Gln 365	1106
ATG Met	ACA Thr	GCT Ala	GAG Glu	GTA Val 370	GCA Ala	CGA Arg	TTT Phe	AGG Arg	TAC Tyr 375	ATT Ile	CAA Gln	AAC Asn	TTG Leu	GTA Val 380	ACT Thr	1154
AAG Lys	AAC Asn	TTC Phe	CCC Pro 385	AAC Asn	AAG Lys	TTC Phe	GAC Asp	TCG Ser 390	GAT Asp	AAC Asn	AAG Lys	GTG Val	ATT Ile 395	CAA Gln	TTT Phe	1202
		AGC Ser 400				Ile										1250
AAC	GGC	GTG	TTT	AAT	AAA	GAT	TAT	GAT	TTC	GGG	TTT	GGA	AAA	GTG	AGG	1298

Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg 415 420 425	
CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro 430 435 440 445	1346
AAG TAGTCAAACG AGGCCTGCAG Lys	1369
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 30 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
CATATGTGTGTCACATCACATTAGAT	30
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
CAGGTTTGGA TCCTTTACGT T	21
(2) INFORMATION FOR SEQ ID NO:36:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 82 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36	
AAGGAGATATACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC Met Gly Ser Ser His His His His His Ser Ser	43
GGC CTG GTG CCG CGC GGC AGC CAT ATG CTC GAG GAT CCG Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro 15 20 25	82
(2) INFORMATION FOR SEQ ID NO:37:	

	,			•	
		(A)	LENGTH: 23 base pairs		
		(B)	TYPE: nucleic acid		
		(C)	STRANDEDNESS: single		
			TOPOLOGY: linear		
	(ii)	MOLE	ECULE TYPE: DNA (genomic)		
	(xi)	SEQU	JENCE DESCRIPTION: SEQ ID NO:37	•	
AAA	CAAC	GTAAA	AGA TCCAAA CCTGAAA		23
701			· ·		
(2)	INFO	KMATI	ON FOR SEQ ID NO:38:		
-	( <u>i</u> )	SEQU	JENCE CHARACTERISTICS:		
		(A)	LENGTH: 36 base pairs		
			TYPE: nucleic acid		
		(C)	STRANDEDNESS: single		
			TOPOLOGY: linear		
*					
	(ii)	MOLE	CULE TYPE: DNA (genomic)		
	1:1	222.0	WTD D	•	
	(IX)	FEAT	NAME/KEY: CDS		
			LOCATION: 335		
			NAME/KEY: Cathepsin B linker		
		(4)	MANE/REI: Cachepsin B linker		
	(xi)	SEQU	ENCE DESCRIPTION: SEQ ID NO:38		
CCA	rGGCC	CT GG	CCCTGGCC CTGGCCCTGG CCATGG		36
(2)	INFO	TTAMS	ON FOR SEQ ID NO:39:		
,			on 10x 02g 20 x0.33.		
	(i)	SEQU	ENCE CHARACTERISTICS:		
			LENGTH: 51 base pairs		
		(B)	TYPE: nucleic acid		
		(C)	STRANDEDNESS: single		
		(D)	TOPOLOGY: linear	•	
	1221				
	(11)	MOLE	CULE TYPE: DNA (genomic)		
	(ix)	FEAT	URE:		
		(A)	NAME/KEY: CDS	•	
			LOCATION: 350		
			NAME/KEY: Cathepsin D linker		
	(xi)	SEQU	ENCE DESCRIPTION: SEQ ID NO:39		
		ac		compaga a su ma c	<b>5</b> 3
CCAT	الافاقات	LG AT	CGGGCTTC CTGGGCTTCG GCTTCCTGGG	CITCGCCAIGG	51
(2)	INFO	RMATI	ON FOR SEQ ID NO:40:		
,				-	
	(i)	SEQU	ENCE CHARACTERISTICS:		

(A) LENGTH: 27 base pairs

PCT/US95/10973

(ii) MOLECULE TYPE: DNA (genomic)	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 326     (A) NAME/KEY: Gly4Ser with Ncol ends</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40	
CCATGGGCGG CGGCGGCTCT GCCATGG	27
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 42 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(ix) FEATURE:  (A) NAME/KEY: CDS  (B) LOCATION: 341  (A) NAME/KEY: (Gly4Ser)2 with Ncol ends	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41	
CCATGGGCGG CGGCGGCTCT GGCGGCGGCG GCTCTGCCAT GG 4	2
(2) INFORMATION FOR SEQ ID NO:42:	
<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 75 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
(ii) MOLECULE TYPE: DNA (genomic)	
<pre>(ix) FEATURE:     (A) NAME/KEY: CDS     (B) LOCATION: 374     (A) NAME/KEY: (Ser4Gly)4 with NcoI ends</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42	
CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCTC GTCGTCGTCGT	60
CGTCGGGCGC CATGG	<b>75</b>

(2)	INFO	DRMATION FOR SEQ ID NO:43:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 45 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURE:	
		(A) NAME/KEY: CDS	
		(B) LOCATION: 345	
		(A) NAME/KEY: (Ser <sub>4</sub> Gly) <sub>2</sub>	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:43	
CCAT		TC GTCGTCGTCG GGCTCGTCGT CGTCGGGCGC CATGG	4-
			4.5
(2)	INFO	RMATION FOR SEQ ID NO:44:	
	(i)	SEQUENCE CHARACTERISTICS:	
	•	(A) LENGTH: 96 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: DNA (genomic)	
	(ix)	FEATURE:	
	,	(A) NAME/KEY: CDS	
		(B) LOCATION: 395	
		(A) NAME/KEY: "Trypsin linker"	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:44	
CAT	GGGC	EG ATCGGGCGGT GGGTGCGCTG GTAATAGAGT CAGAAGATCA GTCGGAAGCA	60
CCT	GTCT	TG CGGTGGTCTC GACCTGCAGG CCATGG	96
2)	INFO	RMATION FOR SEQ ID NO:45:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 18 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: double	
		(D) TOPOLOGY: unknown	
	(ii)	MOLECULE TYPE: cDNA	٠
	(ix)	FEATURE:	
		(A) NAME/KEY: CDS	
		(B) LOCATION: 118	
		(D) OTHER INFORMATION: /product= Thrombin substrate linker	
		· · · · · · · · · · · · · · · · · · ·	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45 CTG GTG CCG CGC GGC AGC 18 Leu Val Pro Arg Gly Ser . 5 (2) INFORMATION FOR SEQ ID NO:46: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown . (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..15 (D) OTHER INFORMATION: /product= Enterokinase substrate linker (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46 GAC GAC GAC CCA 15 Asp Asp Asp Lys 1 (2) INFORMATION FOR SEQ ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: unknown (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1..12 (D) OTHER INFORMATION: /product= Factor Xa substrate (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47 ATC GAA GGT CGT 12 Ile Glu Gly Arg (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 8 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: peptide
```

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..8

(D) OTHER INFORMATION: /product= Flexible linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

Ala Ala Pro Ala Ala Ala Pro Ala

- (2) INFORMATION FOR SEQ ID NO:49:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..4
    - (D) OTHER INFORMATION: /product= subtilisin substrate linker
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49 Phe Ala His Tyr 1

- (2) INFORMATION FOR SEQ ID NO:50:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 4 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..4
    - (D) OTHER INFORMATION: /product= subtilisin substrate linker
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

Xaa Asp Glu Leu

1

(2) INFORMATION FOR SEQ ID NO:51:

	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 26 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear			
	(ii)	MOLECULE TYPE: cDNA			
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:51		·	
CAT	GGCA	CC AATGGCAGAA GGAGGA			26
(2)	INFO	RMATION FOR SEQ ID NO:52:			
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: unknown			
	(ii)	MOLECULE TYPE: cDNA			
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:52			
TCG	ACTC	AT CACCGCCTCG GCTT			24
(2)	INFO	RMATION FOR SEQ ID NO:53:	***		
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 38 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: unknown			
	(ii)	MOLECULE TYPE: cDNA	•		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:53			
CAI	regec	G CGGCGGCTCT GCACCAATGG CAGAAGGA			38
(2)	INFO	RMATION FOR SEQ ID NO:54:			
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 53 bases  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: unknown			
	(ii)	MOLECULE TYPE: cDNA			
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:54			
CCA1	rgggc	G CGGCGGCTCT GGCGGCGGCG GCTCTGCACC	AATGGCAGAA	GGA	53

(2)	INFO	ORMA:	CION FO	R SE	Q ID	NO:	55:									
	(i)	() (E	QUENCE A) LENG B) TYPE C) STRA D) TOPO	TH: 4 : nuc NDEDI	il ba cleid NESS:	ases c ac: : do:	id ıble									
	(ii)	MOI	ECULE	TYPE:	cD1	AI										
	(xi)	SEC	UENCE	DESC	RIPTI	ON:	SEQ	ID N	<b>1</b> 0 : 55	5						
CCA	TGGCA	AGA G	CCGCCG	CCG (	ccce	CCTC	G GC	TTGI	CACA	T					41	
(2)	INFO	RMAT	ION FO	R SEC	) ID	NO:5	6:									
	(i)	(A (B (C	UENCE LENG TYPE STRA	TH: 5 : nuc NDEDN	6 ba leic ESS:	ses aci	.d gle									
	(ii)	MOL	ECULE	TYPE:			•									
	(xi)	SEQ	UENCE :	DESCR	IPTI	ON:	SEQ	ID N	0:56						٠	
			CCGCCG					CCGC	cccg	CCT	ceec	TTG	TCAC	AT	56	
	(i)	(A (B (C	UENCE ( ) LENG: ) TYPE ) STRAI ) TOPOI	TH: 1 : nuc VDEDN	167 : leic ESS:	base aci sin	pai d gle	rs				-				
	(ii)	MOL	ECULE :	TYPE:	cDN.	A										
	(ix)	(A)	TURE: ) NAME; ) LOCAT ) OTHER	: NOI	4		: /p:	rodu	ct= '	"SAP	- (G1	y4Se:	r)-V	EGF121	••	
	(xi)	SEQ	UENCE I	ESCR	IPTI	ON:	SEQ :	ID N	D:57	:						
CAT			ACA TCA Thr Sea													48
AA Sln	TAC T	CA :	CT TTT Ser Phe	Val	GAT Asp	AAA Lys	ATC Ile	CGA Arg	AAC Asn	AAC Asn	GTA Val	AAG Lys	GAT Asp	CCA Pro		96

AAC Asn	CTG Leu	AAA Lys	TAC Tyr 35	GGT Gly	GGT Gly	ACC Thr	GAC Asp	ATA Ile 40	GCC	GTG Val	ATA Ile	GGC	CCA Pro 45	CCT Pro	TCT Ser	144
AAA Lys	GAA Glu	AAA Lys 50	TTC Phe	CTT Leu	AGA Arg	ATT Ile	AAT Asn 55	TTC Phe	CAA Gln	AGT Ser	TCC Ser	CGA Arg 60	GGA Gly	ACG Thr	GTC Val	192
TCA Ser	CTT Leu 65	GGC Gly	CTA	AAA Lys	CGC <b>Ar</b> g	GAT Asp 70	AAC Asn	TTG Leu	TAT Tyr	GTG Val	GTC Val 75	GCG Ala	TAT	CTT Leu	GCA Ala	240
ATG Met 80	GAT Asp	AAC Asn	ACG Thr	AAT Asn	GTT Val 85	AAT Asn	CGG Arg	GCA Ala	TAT	TAC Tyr 90	TTC Phe	AAA Lys	TCA Ser	GAA Glu	ATT Ile 95	288
ACT	TCC Ser	GCC Ala	GAG Glu	TTA Leu 100	ACC Thr	GCC Ala	CTT Leu	TTC Phe	CCA Pro 105	GAG Glu	GCC Ala	ACA Thr	ACT Thr	GCA Ala 110	AAT Asn	336
CAG Gln	AAA Lys	GCT Ala	TTA Leu 115	GAA Glu	TAC Tyr	ACA Thr	GAA Glu	GAT Asp 120	TAT	CAG Gln	TCG Ser	ATC Ile	GAA Glu 125	AAG Lys	AAT Asn	384
GCC Ala	Gln	ATA Ile 130	ACA Thr	CAG Gln	GGA Gly	GAT Asp	AAA Lys 135	AGT Ser	AGA Arg	AAA Lys	GAA Glu	CTC Leu 140	GGG Gly	TTG Leu	GGG	432
ATC Ile	GAC Asp 145	TTA Leu	CTT Leu	TTG Leu	ACG Thr	TTC Phe 150	ATG Met	GAA Glu	GCA Ala	GTG Val	AAC Asn 155	AAG Lys	AAG Lys	GCA Ala	CGT Arg	480
GTG Val 160	GTT Val	AAA Lys	AAC Asn	GAA Glu	GCT Ala 165	AGG Arg	TTT Phe	CTG Leu	CTT Leu	ATC Ile 170	GCT Ala	ATT	CAA Gln	ATG Met	ACA Thr 175	528
GCT Ala	GAG Glu	GTA Val	GCA Ala	CGA Arg 180	TTT Phe	AGG Arg	TAC Tyr	ATT Ile	CAA Gln 185	AAC Asn	TTG Leu	GTA Val	ACT Thr	AAG Lys 190	AAC Asn	576
					GAC Asp											624
					TCT Ser											672
					TAT Tyr					Gly						720
					GGA Gly											768

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240					245					250					255	
															GGG	816
Met	GIY	GIA	GIY	260	ser	Ala	Met	Ala	Pro 265	Met	Ala	Glu	Gly	Gly 270	Gly	
															AGC	864
Gln	Asn	His	His 275	Glu	Val	Val	Lys	Phe 280	Met	qaA	Val	Tyr	Gln 285	Arg	Ser	
															CCT	912
Tyr	Cys	His 290	Pro	Ile	Glu	Thr	Leu 295	Val	qaA	Ile	Phe	Gln 300	Glu	Tyr	Pro	
			GAG													960
Asp	Glu 305	Ile	Glu	Tyr	Ile	Phe 310	Lys	Pro	Ser	Суѕ	Val 315	Pro	Leu	Met	Arg	
			TGC													1008
Cys 320	Gly	Gly	Сув	Cys	Asn 325	Asp	Glu	Gly	Leu	Glu 330	Cys	Val	Pro	Thr	Glu 335	
GAG	TCC	AÃC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	ATC	AAA	CCT	CAC	CAA	GGC	1056
Glu	Ser	Asn	Ile	Thr 340		Gln	Ile	Met	Arg 345	Ile	Lys	Pro	His	Gln 350	Gly	
CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	CAC	AAC	AAA	TGT	GAA	TGC	1104
Gln	His	Ile	Gly 355	Glu	Met	Ser	Phe	Leu 360	Gln	His	naA	Lys	Cys 365	Glu	Сув	
AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	AAA	TGT	GAC	AAG	CCG	AGG	1152
Arg	Pro	Lys 370	Lys	Asp	Arg	Ala	<b>Arg</b> 375	Gln	Glu	Lys	Cys	<b>Asp</b> 380	Lys	Pro	Arg	
CGG Arg	TGAT	rgagi	rcg <i>i</i>	C											-	1167

## (2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1299 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 4..1287
  - (D) OTHER INFORMATION: /product= "SAP-(Gly4Ser)-VEGF165"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

	,				 	 	•	,		
CAT		GTC Val								48
		TCA Ser								96
		AAA Lys								144
		AAA Lys 50								192
		GGC Gly								240
		AAC Asn								288
		GCC Ala								336
		GCT Ala								384
		ATA Ile 130								432
		TTA	-							480
		AAA Lys								528
		GTA Val								576
		AAC Asn				Lys				624

			Lys			ACG Thr									GGC Gly	672
GTG Val	TTT Phe 225	AAT Asn	AAA Lys	GAT Asp	TAT	GAT Asp 230	TTC Phe	GGG Gly	TTT	GGA Gly	AAA Lys 235	GTG Val	AGG Arg	CAG Gln	GTG Val	720
AAG Lys 240	GAC Asp	TTG Leu	CAA Gln	ATG Met	GGA Gly 245	CTC Leu	CTT Leu	ATG Met	TAT	TTG Leu 250	GGC Gly	AAA Lys	CCA Pro	AAG Lys	GCC Ala 255	768
						GCC Ala										816
						GTG Val										864
						ACC Thr										912
						TTC Phe 310										960
						GAC Asp										1008
						CAG Gln										1056
						AGC Ser										1104
						GCA Ala										1152
						TTG Leu 390										1200
						GAC Asp										1248
						AGA Arg							TGAT	GAGT	CG	1297

AC 1299

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..771
- (D) OTHER INFORMATION: /product= "SAP CYS -1"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

														ACC Thr		48
					-									AAG Lys 30		96
														CCA Pro		144
														GGA Gly		192
														TAT Tyr		240
														TCA Ser		288
														ACT Thr 110	GCA Ala	336
AAT Asn	CAG Gln	AAA Lys	GCT Ala 115	TTA Leu	GAA Glu	TAC Tyr	ACA Thr	GAA Glu 120	Asp	TAT Tyr	CAG Gln	TCG Ser	ATC Ile 125	GAA Glu	AAG Lys	384

AAT Asn	GCC Ala	Gln 130	Ile	ACA Thr	CAG Gln	GGA Gly	GAT Asp 135	AAA Lys	AGT Ser	AGA Arg	AAA Lys	GAA Glu 140	CTC	GGG	TTG Leu	432
GGG	ATC Ile 145	GAC Asp	TTA Leu	CTT Leu	TTG Leu	ACG Thr 150	TTC Phe	ATG Met	GAA Glu	GCA Ala	GTG Val 155		AAG Lys	AAG Lys	GCA Ala	480
CGT Arg 160	GTG Val	GTT Val	AAA Lys	AAC Asn	GAA Glu 165	GCT Ala	AGG Arg	TTT Phe	CTG Leu	CTT Leu 170	ATC Ile	GCT Ala	ATT Ile	CAA Gln	ATG Met 175	528
ACA Thr	GCT Ala	GAG Glu	GTA Val	GCA Ala 180	CGA Arg	TTT Phe	AGG Arg	TAC	ATT Ile 185	CAA Gln	AAC Asn	TTG Leu	GTA Val	ACT Thr 190	AAG Lys	576
AAC Asn	TTC Phe	CCC Pro	AAC Asn 195	AAG Lys	TTC Phe	GAC Asp	TCG Ser	GAT Asp 200	AAC Asn	AAG Lys	GTG Val	ATT Ile	CAA Gln 205	TTT Phe	GAA Glu	624
GTC Val	AGC Ser	TGG Trp 210	CGT Arg	AAG Lys	ATT Ile	TCT Ser	ACG Thr 215	GCA Ala	ATA Ile	TAC Tyr	GGG Gly	GAT Asp 220	GCC Ala	AAA Lys	AAC Asn	672
GGC Gly	GTG Val 225	TTT Phe	AAT Asn	AAA Lys	Asp	TAT Tyr 230	GAT Asp	TTC Phe	GGG Gly	TTT Phe	GGA Gly 235	AAA Lys	GTG Val	AGG Arg	CAG Gln	720
GTG Val 240	AAG Lys	GAC Asp	TTG Leu	Gln	ATG Met 245	GGA Gly	CTC . Leu	CTT Leu	Met	TAT Tyr 250	TTG Leu	GGC Gly	AAA Lys	Pro	AAG Lys 255	768
TAG					-											771

- (2) INFORMATION FOR SEQ ID NO:60:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

## TCCCAGGCTG CACCAATGGC AGAAGGAGGA

- (2) INFORMATION FOR SEQ ID NO:61:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

WO 96/06641 PCT/US95/109

		(D) :	POPOLOGY:	linear						
	(ii)	MOLECT	JLE TYPE:	CDNA						
	(ix)	(B) 1	NAME/KEY: LOCATION:	1-9	/product=	"3'	linking	oligo	for	insertio
into	0 11a,				•		-	_		
	(xi)	SEQUE	NCE DESCR	RIPTION: S	EQ ID NO:6	1:				
TCC	CCTT	CT GCC	ATTGGTG (	CAGCCTGGGA						30
(2)	INFO	CITAMS	N FOR SEC	ID NO:62	:					
	(i)	(A) (B) (C)	LENGTH: 2 TYPE: nuc STRANDED!	ACTERISTIC 24 base pa cleic acid VESS: sing : linear	irs					
	(ii)	MOLEC	ULE TYPE:	CDNA						
	(xi)	SEQUE	NCE DESC	RIPTION: S	EQ ID NO:6	2:				
CAT	ATGAA	TTC:	rectete 1	TTGG						24
(2)	INFO	CITAMS	N FOR SEC	ID NO:63	:					
	(i)	(A) (B) (C)	LENGTH: 2 TYPE: nuc	ACTERISTIC 29 base pa cleic acid WESS: sing	irs					
	(ii)	MOLEC	ULE TYPE	: cDNA						
	(xi)	SEQUE	NCE DESCI	RIPTION: S	EQ ID NO:6	3 :				
CAT	ATGGC	AC CAA	TGGCAGA J	AGGAGGAGG						29
(2)	INFO	RMATIO	N FOR SE	Q ID NO:64	:					
	(i)	(A) : (B) : (C)	LENGTH: :	ACTERISTIC 24 base pa cleic acid NESS: sing : linear	irs					
	(ii)	MOLEC	ULE TYPE	: cDNA	·		•			
	(xi)	SEQUE	NCE DESC	RIPTION: S	EQ ID NO:6	4:				
GGA	TCCTC	AT CAC	CGCCTCG	SCTT						24

(2)	INFO	RMATION FOR SEQ ID NO:65:		
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:65:		
CCA	TGGCC	GC CTCGGCTTGT C		21
(2)	INFO	RMATION FOR SEQ ID NO:66:		
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 29 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:66:		
GGA:	TCCGA	AA CATGAACTTT CTGCTGTCT	·	29
(2)	INFO	RMATION FOR SEQ ID NO:67:		
		SEQUENCE CHARACTERISTICS:  (A) LENGTH: 31 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA	-	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:67:		
GGA:	CCGA	AA CATATGAACT TTCTGCTGTC T		31
(2)	INFO	RMATION FOR SEQ ID NO:68:		
	(i)	SEQUENCE CHARACTERISTICS:  (A) LENGTH: 24 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA		
	,			

CTG	CAGTCAT CACCGCCTCG GCTT	24
(2)	INFORMATION FOR SEQ ID NO:69:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 36 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	·
CAT	ATGGTCA CATCATGTAC ATTAGATCTA GTAAAT	36
(2)	INFORMATION FOR SEQ ID NO:70:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 50 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
CAT	PATGGTCA CATCAATCAC ATTAGATCTA GTATGTCCGA CCGCGGGTCA	50
(2)	INFORMATION FOR SEQ ID NO:71:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 23 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: cDNA	٠.
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
CTG	GCAGGCCT CGTTTGACTA CTT	23
(2)	INFORMATION FOR SEQ ID NO:72:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 7 amino acids</li> <li>(B) TYPE: amino acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: unknown</li> </ul>	
	(ii) MOLECULE TYPE: peptide	
	(ix) FEATURE:	

	(A) NAME/KEY: CDS	
	(B) LOCATION: 17	
	(D) OTHER INFORMATION: /product= nuclear translocation	sequence
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72	
_	•	
	Pro Arg Arg Lys Leu	-
1	5	
4-5		
(2)	INFORMATION FOR SEQ ID NO:73:	
	(i) CECUTAGE CUADACTEDITOTICS	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 28 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(11) MOLECULE TIPE: CDRA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:/3:	
الملمك	AGGTTT GGATCTTTTA CGTTGTTT	28
(2)	INFORMATION FOR SEQ ID NO:74:	•
(2)	INFORMATION FOR BEG 1D NO.74.	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	- (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(5)	
	(ii) MOLECULE TYPE: cDNA	
	1201 100000000 20001	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
	The second secon	
GGAT	CCGCCT CGTTTGACTA CTT	23
(2)	INFORMATION FOR SEQ ID NO:75:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 6 amino acids	
	(B) TYPE: amino acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: unknown	
	(ii) MOLECULE TYPE: peptide	
	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 16	
	(D) OTHER INFORMATION: /product= nuclear translocation	sequence

Ile Lys Arg Leu Arg Arg

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

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- (2) INFORMATION FOR SEQ ID NO:76:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..6
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

Ile Lys Arg Gln Arg Arg

- (2) INFORMATION FOR SEQ ID NO:77:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 40 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (D) OTHER INFORMATION: /product= "SO-4"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Ile Ty Glu Leu Asn Leu Gln Gly Thr Thr Lys Ala Gln Tyr
5 10 15

Ser Thr Ile Leu Lys Gln Leu Arg Asp Asp Ile Lys Asp Pro Asn Leu 20 25 30

Xaa Tyr Gly Xaa Xaa Asp Tyr Ser 35 40

- (2) INFORMATION FOR SEQ ID NO:78:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1545 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..1545

(D) OTHER INFORMATION: /product=

"SAP- (Gly4Ser) -VEGF121- (Gly4Ser) -VEGF121"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAT	ATG Met	GTC Val	ACA Thr	TCA Ser	ATC Ile 5	ACA Thr	TTA Leu	GAT Asp	CTA Leu	GTA Val 10	AAT Asn	CCG Pro	ACC	GCG Ala	GGT Gly 15	. 48
CAA Gln	TAC	TCA Ser	TCT Ser	TTT Phe 20	GTG Val	GAT Asp	AAA Lys	ATC Ile	CGA Arg 25	AAC Asn	AAC Asn	GTA Val	AAG Lys	GAT Asp 30	CCA Pro	96
AAC Asn	CTG Leu	AAA Lys	TAC Tyr 35	GGT Gly	GGT Gly	ACC Thr	GAC Asp	ATA Ile 40	GCC Ala	GTG Val	ATA Ile	GGC	CCA Pro 45	CCT Pro	TCT Ser	144
AAA Lys	GAA Glu	AAA Lys 50	TTC Phe	CTT Leu	AGA Arg	ATT Ile	AAT Asn 55	TTC Phe	CAA Gln	AGT Ser	TCC Ser	CGA Arg 60	GGA Gly	ACG Thr	GTC Val	192
TCA Ser	CTT Leu 65	GGC	CTA Leu	AAA Lys	CGC	GAT Asp 70	AAC Asn	TTG Leu	TAT Tyr	GTG Val	GTC Val 75	GCG Ala	TAT Tyr	CTT Leu	GCA Ala	240
ATG Met 80	GAT Asp	AAC Asn	ACG Thr	AAT Asn	GTT Val 85	AAT Asn	CGG Arg	GCA Ala	TAT Tyr	TAC Tyr 90	TTC Phe	AAA Lys	TCA Ser	G <b>A</b> A Glu	ATT Ile 95	288
ACT Thr	TCC Ser	GCC Ala	GAG Glu	TTA Leu 100	ACC Thr	GCC Ala	CTT Leu	TTC Phe	CCA Pro 105	GAG Glu	GCC Ala	ACA Thr	ACT Thr	GCA Ala 110	TAA naA	336
CAG Gln	AAA Lys	GCT Ala	TTA Leu 115	GAA Glu	TAC Tyr	ACA Thr	GAA Glu	GAT Asp 120	TAT Tyr	CAG Gln	TCG Ser	ATC Ile	GAA Glu 125	AAG Lys	AAT Asn	384
														TTG Leu		432
ATC Ile	GAC Asp 145	TTA Leu	CTT Leu	TTG Leu	ACG Thr	TTC Phe 150	ATG Met	GAA Glu	GCA Ala	GTG Val	AAC Asn 155	AAG Lys	AAG Lys	GCA Ala	CGT Arg	480
														ATG Met		528

			Ala		TTT Phe											576
					GAC Asp											624
					TCT Ser											672
					TAT Tyr											720
					GGA Gly 245											768
	Gly				TCT Ser											816
					GTG Val											864
			Pro		GAG Glu											912
GAT	GAG Glu 305	Ile	GAG Glu	TAC	ATC Ile	TTC Phe 310	Lys	CCA Pro	TCC Ser	TGT Cys	GTG Val 315	Pro	CTG Leu	ATG Met	CGA Arg	960
TGC Cys 320	Gly	GGC	TGC Cys	TGC Cys	AAT Asn 325	GAC Asp	GAG Glu	GGC Gly	CTG Leu	GAG Glu 330	Сув	GTG Val	CCC Pro	ACT Thr	GAG Glu 335	1008
GAG Glu	TCC Ser	AAC Asn	: ATC	Thr	Met	CAG Gln	ATT	Met	CGG Arg 345	Ile	Lys	CCT Pro	CAC His	CAA Gln 350	GGC Gly	1056
CAG Glr	CAC His	ATA	GGA Gly 355	Glu	ATG Met	AGC Ser	TTC Phe	CTA Leu 360	Glr	CAC His	AAC Asn	AAA Lys	TGT Cys	Glu	TGC	1104
AGA	CC#	AAC Lys 370	Lys	GAT qea	AGA Arg	GCA Ala	AGA Arg 379	, Glr	A GAA	AAA Lys	TGI Cys	GAC Asp 380	Lys	CCG Pro	AGG Arg	1152
Arg	G GCC G Ala 389	a Met	G GGC	GGC Gly	GGC Gly	GGC Gly 390	/ Ser	C Ala	ATC A Met	GCA Ala	A CCA Pro 395	Met	GCA Ala	GAA	GGA Gly	1200

159

GGA Gly 400	Gly	CAG Gln	AAT Asn	CAT His	CAC His 405	GAA Glu	GTG Val	GTG Val	AAG Lys	Phe	Met	GAT Asp	GTC Val	TAT	CAG Gln 415	1248
CGC Arg	AGC Ser	TAC Tyr	TGC Cys	CAT His 420	CCA Pro	ATC Ile	GAG Glu	ACC Thr	CTG Leu 425	GTG Val	GAC	ATC Ile	TTC Phe	CAG Gln 430	GAG Glu	1296
TAC Tyr	CCT	GAT Asp	GAG Glu 435	ATC Ile	GAG Glu	TAC Tyr	ATC Ile	TTC Phe 440	AAG Lys	CCA Pro	TCC Ser	TGT Cys	GTG Val 445	CCC	CTG Leu	1344
ATG Met	CGA Arg	TGC Cys 450	GGG Gly	GGC Gly	TGC Cys	TGC Cys	AAT Asn 455	GAC Asp	GAG Glu	GGC Gly	CTG Leu	GAG Glu 460	TGT Cys	GTG Val	CCC Pro	1392
ACT Thr	GAG Glu 465	GAG Glu	TCC Ser	AAC Asn	ATC Ile	ACC Thr 470	ATG Met	CAG Gln	ATT Ile	ATG Met	CGG Arg 475	Ile	AAA Lys	CCT Pro	CAC His	1440
CAA Gln 480	GGC Gly	CAG Gln	CAC His	Ile	GGA Gly 485	GAG Glu	ATG Met	AGC Ser	TTC Phe	CTA Leu 490	CAG Gln	CAC His	AAC Asn	AAA Lys	TGT Cys 495	1488
GAA Glu	TGC Cys	AGA Arg	CCA Pro	AAG Lys 500	AAA Lys	GAT Asp	AGA Arg	GCA Ala	AGA Arg 505	CAA Gln	GAA Glu	AAA Lys	TGT Cys	GAC Asp 510	AAG Lys	1536
	AGG Arg	CGG Arg	TGAT	GAGT	CG A	.c									. 1º +	1557

## (2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1809 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 4..1797
  - (D) OTHER INFORMATION: /product=
    "SAP-(Gly4Ser)-VEGF165"
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:
- CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly

•	1				5					10					15	
	_				_											
CAA	TAC	TCA	TCT	TTT	GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	9
Gln	Tyr	Ser	Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	
	•			20					25					30		
220	CTG	222	TAC	CCT	CCT	200	GNC	እሞአ	ccc	CTC	3003		001		TCT	1.4
															Ser	14
		_,_	35	,	,		p	40	~	141	116	GIY	45	710	261	
AAA	GAA	AAA	TTC	CTT	AGA	ATT	AAT	TTC	CAA	AGT	TCC	CGA	GGA	ACG	GTC	19:
					Arg											
		50				~	55	•	٠	•		60				•
TCA	CTT	GGC	CTA	AAA	CGC	GAT	AAC	TTG	TAT	GTG	GTC	GCG	TAT	CTT	GCA	240
															Ala	
	65					70					75					
															ATT	286
	Asp	Asn	Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Lys	Ser	Glu	Ile	
80					85					90					95	
ACT	TCC	GCC	GAG	TTA	ACC	GCC	CTT	TTC	CCA	GAG	GCC	ACA	ACT	GCA	AAT	336
					Thr											
				100		-			105					110		
CAG	AAA	GCT	TTA	GAA	TAC	ACA	GAA	GAT	TAT	CAG	TCG	ATC	GAA	AAG	AAT	384
					Tyr											
			115					120					125			
GCC	CAG	ATA	ACA	CAG	GGA	GAT	AAA	AGT	AGA	AAA	GAA	CTC	GGG	TTG	GGG	432
Ala	Gln	Ile	Thr	Gln	Gly	Asp	Lys	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	
		130					135					140				
ATC	GAC	TTA	CTT	TTG	ACG	TTC	ATG	GAA	GCA	GTG	AAC	AAG	AAG	GCA	CGT	480
Ile	Asp	Leu	Leu	Leu	Thr	Phe	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	
	145					150					155					
GTG	GTT	AAA	AAC	GAA	GCT	AGG	TTT	CTG	CTT	ATC	GCT	ATT	CAA	ATG	ACA	528
Val	Val	Lys	Asn	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	
160					165					170					175	
GCT	GAG	GTA	GCA	CGA	TTT	AGG	TAC	ATT	CAA	AAC	TTG	GTA	ACT	AAG	AAC	576
Ala	Glu	Val	Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Thr	Lys	Asn	
				180					185					190		
TTC	CCC	AAC	AAG	TTC	GAC	TCG	GAT	AAC	AAG	GTG	ATT	CAA	TTT	GAA	GTC	624
Phe	Pro	Asn	Lys	Phe	Asp	Ser	Asp	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	
			195					200					205			
AGC	TGG	CGT	AAG	ATT	TCT	ACG	GCA	ATA	TAC	GGG	GAT	GCC	AAA	AAC	GGC	672
					Ser											_
		210					215			-	-	220			_	
GTG	ىلىنىڭ	דעע	444	TAD	тат	ТДЭ	<del>ተ</del>	GGG		GGA	מממ	GTG	<b>V</b> GC	CAG	GTG	720

Va.	l Ph 22	e As 5	n Ly	s As	р Ту	r As <sub>j</sub> 23(	Pho	e Gl	y Ph	e Gl	y Ly 23		l Ar	g Gl	n Val	
AA( Lys 24(	S AS	C TT p Le	G CA u Gl:	A ATO	G GG/ E Gl <sub>3</sub> 245	/ Let	CT.	r ATC	TA:	T TT( r Let 25(	ı Gl	C AAI y Lyi	A CCI	A AA	G GCC 5 Ala 255	
ATC Met	GG(	GG GG G1	C GG y Gl	260 260	/ Ser	GCA Ala	CC#	A ATO	GCI Ala 265	Glu	GG Gl	A GGJ Y Gly	GG( Gl <sub>y</sub>	Gl:	G AAT n Asn	816
CAT His	CAC His	GA Gli	A GT( u Val 275	L Val	Lys	TTC Phe	ATG Met	GAT Asp 280	Val	TAI	CAC Glr	G CGC	AGC Ser 285	Tyz	TGC Cys	864
CAT His	Pro	AT(	e GIL	ACC Thr	CTG Leu	GTG Val	GAC Asp 295	Ile	TTC	CAG Gln	GAG Glu	TAC Tyr 300	Pro	GAT Asp	GAG Glu	912
ATC	GAG Glu 305	Туз	Ile	TTC Phe	AAG Lys	CCA Pro 310	TCC Ser	TGT Cys	GTG Val	CCC	CTG Leu 315	Met	CGA Arg	TGC	GGG Gly	960
GGC Gly 320	CAB	TGC	TAA :	GAC Asp	GAG Glu 325	GGC Gly	CTG Leu	GAG Glu	TGT Cys	GTG Val 330	CCC Pro	ACT Thr	GAG Glu	GAG Glu	TCC Ser 335	1008
AAC Asn	ATC Ile	ACC	Met	CAG Gln 340	ATT Ile	ATG Met	CGG Arg	ATC Ile	AAA Lys 345	CCT Pro	CAC His	CAA Gln	GGC Gly	CAG Gln 350	CAC His	1056
ATA Ile	GGA Gly	GAG Glu	ATG Met 355	AGC Ser	TTC Phe	CTA Leu	CAG Gln	CAC His 360	AAC Asn	aaa Lys	TGT Cys	GAA Glu	TGC Cys 365	AGA Arg	CCA Pro	1104
AAG Lys	AAA Lys	GAT Asp 370	AGA Arg	GCA Ala	AGA Arg	CAA Gln	GAA Glu 375	AAT Asn	CCC Pro	TGT Cys	GGG Gly	CCT Pro 380	TGC Cys	TCA Ser	GAG Glu	1152
CGG Arg	AGA Arg 385	AAG Lys	CAT His	TTG Leu	TTT Phe	GTA Val 390	CAA Gln	GAT Asp	CCG Pro	Gln	ACG Thr 395	TGT Cys	AAA Lys	TGT Cys	TCC Ser	1200
TGC Cys 400	AAA Lys	AAC Asn	ACA Thr	GAC Asp	TCG Ser 405	CGT Arg	TGC Cys	AAG Lys	Ala	AGG Arg 410	CAG Gln	CTT Leu	GAG Glu	TTA Leu	AAC Asn 415	1248
GAA Glu	CGT Arg	ACT Thr	TGC Cys	AGA Arg 420	TGT Cys	GAC . Asp :	AAG Lys	Pro .	AGG Arg 425	CGG Arg	GGC Gly	GGC Gly	Gly	GGC Gly 430	TCT Ser	1296
GCC . Ala :	AŢG Met	GCA Ala	CCA Pro 435	ATG Met	GCA Ala	GAA ( Glu (	Gly	GGA ( Gly ( 440	GGG Gly	CAG :	AAT Asn	His :	CAC His	GAA Glu	GTG Val	1344

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GTG Val	AAG Lys	TTC Phe 450	ATG Met	gat Asp	GTC Val	TAT Tyr	CAG Gln 455	CGC Arg	AGC Ser	TAC	TGC Cys	CAT His 460	CCA Pro	ATC Ile	GAG Glu		1392
ACC Thr	CTG Leu 465	GTG Val	GAC Asp	ATC Ile	TTC Phe	CAG Gln 470	GAG Glu	TAC Tyr	CCT	GAT Asp	GAG Glu 475	ATC Ile	GAG Glu	TAC Tyr	ATC Ile		1440
TTC Phe 480	AAG Lys	CCA Pro	TCC Ser	TGT Cys	GTG Val 485	CCC Pro	CTG Leu	ATG Met	CGA Arg	TGC Cys 490	GGG Gly	GGC Gly	TGC Cys	TGC Cys	AAT Asn 495		1488
GAC Asp	GAG Glu	GGC Gly	CTG Leu	GAG Glu 500	TGT Cys	GTG Val	CCC Pro	ACT Thr	GAG Glu 505	GAG Glu	TCC Ser	AAC Asn	ATC Ile	ACC Thr 510	ATG Met		1536
CAG Gln	ATT Ile	ATG Met	CGG Arg 515	ATC Ile	AAA Lys	CCT Pro	CAC His	CAA Gln 520	GGC	CAG Gln	CAC His	ATA Ile	GGA Gly 525	GAG Glu	ATG Met		1584
				CAC His													1632
GCA Ala	AGA Arg 545	CAA Gln	GAA Glu	AAT Asn	CCC Pro	TGT Cys 550	GGG Gly	CCT Pro	TGC Cys	TCA Ser	GAG Glu 555	CGG Arg	AGA Arg	AAG Lys	CAT		1680
TTG Leu 560	TTT Phe	GTA Val	CAA Gln	GAT Asp	CCG Pro 565	CAG Gln	ACG Thr	TGT Cys	AAA Lys	TGT Cys 570	TCC Ser	TGC Cys	AAA Lys	AAC Asn	ACA Thr 575		1728
GAC Asp	TCG Ser	CGT Arg	TGC Cys	AAG Lys 580	GCG Ala	AGG Arg	CAG Gln	CTT Leu	GAG Glu 585	TTA Leu	AAC Asn	GAA Glu	CGT Arg	ACT Thr 590	TGC Cys	:	1776
				CCG Pro			TGAT	'GAGT	CG A	.c						:	1809

30

## (2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

## TGGTCCCAGGCTGCACCC ATGTGTGAAGGAGGAGGGCAGAATCAT

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 bases	
(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	•
<u> </u>	•
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81	
ATG_ATT'CTGCCCTCCTTCACACATG GGTGCAGCCTGGGACCA	30
(2) INFORMATION FOR SEQ ID NO:82:	
(i) SEQUENCE CHARACTERISTICS:	- •
(A) LENGTH: 30 bases	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
122 NOT THE TOTAL TOTAL	uutron.
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82	
GCCAAGTGGTCCCAGG CTGCATGTCCCATGGCAGAAGG AGGAGGGCAG	30
	30
(2) INFORMATION FOR SEQ ID NO:83:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 30 bases	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	979
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: cDNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83	
CTGCCCTCCTCCTCCGCATGGG ACATGCAGCCTGGGACCACTTGGC	30
·	
(2) INFORMATION FOR SEQ ID NO:84:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 5 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: unknown	
(ii) MOLECULE TYPE: peptide	
(ix) FEATURE:	•
(A) NAME/KEY: CDS	
(B) LOCATION: 15	
(D) OTHER INFORMATION: /product= nuclear translocation	sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

Ile Arg Val Arg Arg

1 5

- (2) INFORMATION FOR SEQ ID NO:85:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 6 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..6
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

Lys Arg Lys Arg Lys Lys
1 5

- (2) INFORMATION FOR SEQ ID NO:86:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 467 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 12..455
    - (D) OTHER INFORMATION: /product= "VEGF121 Cys +4"
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:
- GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC 50

  Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala

  1 5 10
- TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC ATG

  15 Pro Met

  20 25
- TGT GCA GAA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG

  146
  Cys Ala Glu Gly Gly Gln Asn His His Glu Val Val Lys Phe Met

30					35					40					45	
GAT	GTC	TAT	CAG	CGC	AGC	TAC	TGC	CAT	CCA	ATC	GAG	ACC	CTG	GTG	GAC	194
Asp	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	
				50					55					60		
ATC	TTC	CAG	GAG	TAC	CCT	GAT	GAG	ATC	GAG	TAC	ATC	TTC	AAG	CCA	TCC	242
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	
			65					70					75			
TGT	GTG	ccc	CTG	ATG	CGA	TGC	GGG	GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	290
Сув	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	
		80					85				•	90				
GAG	TGT	GTG	CCC	ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	338
Glu	Сув	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	
	95				-	100					105					- · ·
ATC	AAA	CCT	CAC	CAA	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	386
															Gln.	
110					115					120					125	4.00
CAC	AAC	AAA	TGT.	GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	434
														Gln		
				130					135					140		
AAA	TGT	GAC	AAG	CCG	AGG	CGG	TGAT	rgac:	rgc z	\G						. 467
		qaA														
			145													
(2)	INFO	RMAT	MOI	FOR	SEQ	ID N	10:87	7 :								
	(i)	SEC	UENC	E CH	LARAC	TER	STIC	?S :								
	•-•	_	-					airs	3							
							acid									
			) TO				sing nown	jle								
		•-														
	(ii)	MOL	ECUI	E TY	PE:	CDNA	<b>,</b>									
	(ix)	FEA														
			) NA													
		-	) LC					/pr	oduc	·t= "	VEGE	7165	Cvs	+4"		
		,_	,					, 5-					-,0	•		
	(~i)	SEC	TENC	r De	CODI	· דידר	N	SEO I	ים איכ							
	(32)	JE(	102146	<i>D</i> E	.J CRI		,	, <u></u> 1	NC					•		•
GGAT	CCGA	AA C													GCC	
			Met		Phe	Let	ı Lev		Trp	Val	. His	Trp		Leu	Ala	
			_	•			-	•								
TTG	CTG	CTC	TAC	CTC	CAC	CAT	GCC	AAG	TGG	TCC	CAG	GCT	GCA	CCC	ATG	98

Leu	Leu 15	Leu	Tyr	Leu	His	His 20	Ala	Lys	Trp	Ser	Gln 25	Ala	Ala	Pro	Met		
	GCA Ala														ATG Met 45		146
	GTC Val																194
	TTC Phe															-	242
	GTG Val																290
	TGT Cys 95																338
	AAA Lys																386
	AAC Asn																434
	CCC Pro																482
	CCG Pro																530
	GCG Ala 175																578
	AGG Arg		TGAT	GACT	GC #	AG		-									599

## (2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 456 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYP	E:	CDNA
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l	ix)	FEATURE:	

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..456
- (D) OTHER INFORMATION: /product= "VEGF121 Cys+2 with Ncol sites"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_recomb
- (B) LOCATION: 1..6
- . (D) OTHER INFORMATION: /note= "Ncol restriction site"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_recomb
- (B) LOCATION: 98..103
- (D) OTHER INFORMATION: /note= "NcoI restriction site"

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GG	ATCC	AAAE	CC 1	ATG . Met .	AAC ' Asn :	Phe	CTG ( Leu I	ETG : Leu ! 5	CT : Ser :	rgg ( rp \	GTG (	CAT His	TGG . Trp 10	AGC (	CTT Leu	48
GC0 Ala	TTO Lev	CTC Lev	. ner	TAC Ty	CTC	CAC His	CAT His	Ala	Lys	TGG	S TC	CAC Gli 25	a Ala	r GCI a Ala	A TGT a Cys	96
Pro	Met 30	GCA Ala	GAA Glu	GGZ Gly	A GGA Gly	GGG Gly 35	GID	AAT Asn	CAT His	CAC His	GAA Glu	. Val	GTC Val	AAG Lys	TTC Phe	144
ATG Met 45	GAT Asp	GTC Val	TAT	CAG Gln	CGC Arg	ser	TAC Tyr	TGC Cys	CAT His	CCA Pro 55	ATC	GAG Glu	ACC Thr	CTG	GTG Val 60	192
GAC Asp	ATC Ile	TTC	CAG Gln	GAG Glu 65	TAC	CCT Pro	GAT Asp	GAG Glu	ATC Ile 70	GAG Glu	TAC Tyr	ATC Ile	TTC Phe	AAG Lys 75	CCA Pro	240
TCC Ser	TGT Cys	GTG Val	CCC Pro 80	CTG Leu	ATG Met	CGA Arg	TGC Cys	GGG Gly 85	GGC Gly	TGC Cys	TGC Cys	AAT Asn	GAC Asp 90	GAG Glu	GGC Gly	288
CTG Leu	GAG Glu	TGT Cys 95	GTG Val	CCC Pro	ACT Thr	GAG Glu	GAG Glu 100	TCC Ser	AAC Asn	ATC Ile	ACC Thr	ATG Met 105	CAG Gln	ATT Ile	ATG Met	336
CGG Arg	ATC Ile 110	AAA Lys	CCT Pro	CAC His	CAA Gln	GGC Gly 115	CAG Gln	CAC His	ATA Ile	GGA Gly	GAG Glu 120	ATG Met	AGC Ser	TTC Phe	CTA Leu	384
CAG	CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	432

Gln 125	His	Asn	Lys	Cys	Glu 130		Arg	Pro	Lys	Lys 135		Arg	, Ala	a Arg	Gln 140		
			Asp	AAG Lys 145													45
(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 8	9 :									
		() () ()	A) L B) T C) S' D) T	CE CI ENGTI YPE: TRANI OPOLO	H: 5 DEDNI DGY:	99 b leic ESS: unk	ase aci sin	pair d gle	s								
	(ii)	MO	LECU	LE T	PE:	cDN	A										
	(ix)	(1	B) L( D) O	AME/I	ON: INF	12.			rodu	Ct= '	"VEG	F165	Cys	+2 <u>w</u>	ith 1	NcoI	
	(ix)	() (I	3) L(	ME/I	ON:	1	5		ote=	"Ncc	oI r	estr	icti	on s	ite"		
		() () ()	3) LO 0) O1	ME/H CATI THER	ON: INFO	97 ORMA	TO2	: /nc				estr	icti	on s	ite"		
GGAT			ATC	Asn	177	CTC	CTO	G TC	r TG(	GTO	G CA	T TGG S Trj	Se:	C CT	r GCC	2	50
														TGT Cys			98
														TTC Phe			146
														GTG Val 60			194
														CCA Pro			242

			65					70					75			
TGT Cys	GTG Val	CCC Pro 80	CTG Leu	ATG Met	CGA Arg	TGC Cys	GGG Gly 85	GGC Gly	TGC Cys	TGC Cys	AAT Asn	GAC Asp 90	GAG Glu	GGC Gly	CTG Leu	290
GAG Glu	TGT Cys 95	GTG Val	CCC Pro	ACT Thr	GAG Glu	GAG Glu 100	TCC Ser	AAC Asn	ATC Ile	ACC Thr	ATG Met 105	CAG Gln	ATT Ile	ATG Met	CGG Arg	338
ATC Ile 110	AAA Lys	CCT Pro	CAC His	CAA Gln	GGC Gly 115	CAG Gln	CAC His	ATA Ile	GGA Gly	GAG Glu 120	ATG Met	AGC Ser	TTC Phe	CTA Leu	CAG Gln 125	386
CAC His	AAC Asn	AAA Lys	TGT Cys	GAA Glu 130	TGC Cys	AGA Arg	CCA Pro	AAG Lys	AAA Lys 135	GAT Asp	AGA Arg	GCA Ala	AGA Arg	CAA Gln 140	GAA Glu	434
		TGT Cys														482
		CAG Gln 160														530
AAG Lys	GCG Ala 175	AGG Arg	CAG Gln	CTT Leu	GAG Glu	TTA Leu 180	AAC Asn	GAA Glu	CGT Arg	ACT Thr	TGC Cys 185	AGA Arg	TGT Cys	GAC Asp	AAG Lys	578
	AGG Arg	CGG Arg	TGAT	GACT	GC A	re.										599
(2)	2) INFORMATION FOR SEQ ID NO:90:															

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..7
  - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

Pro Lys Lys Arg Lys Val Glu

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..8
  - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

Pro Pro Lys Lys Ala Arg Glu Val

- (2) INFORMATION FOR SEQ ID NO:92:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..9
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

Pro Ala Ala Lys Arg Val Lys Leu Asp

- (2) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..5
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

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Lys Arg Pro Arg Pro
1 5
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- (2) INFORMATION FOR SEQ ID NO:94:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..5
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

Lys Ile Pro Ile Lys 1 5

- (2) INFORMATION FOR SEQ ID NO:95:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids
      - (B) TYPE: amino acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..9
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

Gly Lys Arg Lys Arg Lys Ser

- (2) INFORMATION FOR SEQ ID NO:96:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - , (B) TYPE: amino acid
      - (C) STRANDEDNESS: single
      - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

Ser Lys Arg Val Ala Lys Arg Lys leu
1 5

- (2) INFORMATION FOR SEQ ID NO:97:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 9 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..9
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

Ser His Trp Lys Gln Lys Arg Lys Phe 1 5

- (2) INFORMATION FOR SEQ ID NO:98:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 8 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..8
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

Pro Leu Leu Lys Lys Ile Lys Gln
1 5

- (2) INFORMATION FOR SEQ ID NO:99:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..7
  - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

Pro Gln Pro Lys Lys Pro

- (2) INFORMATION FOR SEQ ID NO:100
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 15 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
    - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..15
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

Pro Gly Lys Arg Lys Lys Glu Met Thr Lys Gln Lys Glu Val Pro

- (2) INFORMATION FOR SEQ ID NO:101:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 12 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..12
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101
- Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro
- (2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..7
  - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

Asn Tyr Lys Lys Pro Lys Leu

1 5

- (2) INFORMATION FOR SEQ ID NO:103:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 7 amino acids-
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (ii) MOLECULE TYPE: peptide
  - (ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 1..7
    - (D) OTHER INFORMATION: /product= nuclear translocation sequence
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

His Phe Lys Asp Pro Lys Arg

\\MAIN\GROUP\WP\760100\PZM413PC\SEQUENCE LISTING

#### **Claims**

## We claim:

- A conjugate, comprising a targeted agent and a vascular endothelial cell growth factor (VEGF) polypeptide or a portion thereof, wherein the conjugate binds to a VEGF receptor resulting in internalization of the linked targeted agent.
- 2. A conjugate comprising the following components:  $(VEGF)_n$ ,  $(L)_q$  and  $(targeted agent)_m$ , wherein:

L is a linker;

VEGF is a VEGF monomer or a portion thereof;

at least one VEGF monomer is linked at any residue via (L)q to at least one targeted agent;

m and n, which are selected independently, are at least 1;

q is 0 or more as long as the resulting conjugate binds to the targeted receptor is internalized and delivers the targeted agent; and

the conjugate binds to a receptor that interacts with and internalizes VEGF, whereby the targeted agent(s) is internalized in a cell bearing the receptor.

- 3. The conjugate of claim 2, wherein m and n, which are selected independently, are 1-6.
  - 4. The conjugate of claim 2, wherein n is 1.
  - 5. The conjugate of claim 4, wherein m is 1.
  - 6. The conjugate of claim 2, wherein q is 1.
- 7. The conjugate of claim 2, wherein L is selected from the group consisting of protease substrates, linkers that increase the flexibility of the conjugate, linkers that increase the solubility of the conjugate, photocleavable linkers and acid cleavable linkers.
- 8. A conjugate of any one of claims 1 or 2, wherein a VEGF polypeptide is selected from the group consisting of VEGF<sub>121</sub>, VEGF<sub>120</sub>, VEGF<sub>188</sub>, VEGF<sub>189</sub>, VEGF<sub>164</sub>, VEGF<sub>165</sub>, VEGF<sub>205</sub> and a modified VEGF<sub>121</sub>. VEGF<sub>120</sub>, VEGF<sub>188</sub>, VEGF<sub>189</sub>, VEGF<sub>165</sub>, VEGF<sub>205</sub> or VEGF<sub>206</sub> in which a cysteine

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residue is added or replaces a non-essential amino acid residue within about 20 amino acids of the N-terminus or C-terminus of the monomer.

- 9. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a cytotoxic agent.
- 10. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a ribosome-inactivating protein.
  - 11. The conjugate of claim 10, wherein the targeted agent is a saporin.
- 12. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a nucleic acid.
- 13. The conjugate of any one of claims 1 or 2, wherein the targeted agent is an antisense nucleic acid.
- 14. The conjugate of claim 2, wherein the conjugate is a fusion protein selected from the group consisting of FPVS1, FPSV1, FPSV2, FPSV3, FPSV4, FPSV5, FPSV6, FPSV7, FPSV8, FPSVV1, FPSVV2, FPSVV3, FPSVV4, FPSVV5, FPSVV6, FPSVV7 and FPSVV8.
  - 15. The conjugate of claim 2 that has the formula: targeted agent-(L)q-VEGF-(L)r-VEGF, wherein q and r, which may be the same or different, are 0 or 1.
  - 16. A conjugate that has the formula: (targeted agent)<sub>m</sub>-(L)<sub>q</sub>-(VEGF)<sub>n</sub>, wherein L is a linker;

VEGF is a VEGF monomer or a portion thereof:

at least one VEGF monomer is linked at any residue via  $(L)_q$  to at least one targeted agent;

m and n. which are selected independently, are at least 1;

q is 0 or more as long as the resulting conjugate binds to the targeted receptor is internalized and delivers the targeted agent; and

the conjugate binds to a receptor that interacts with and internalizes VEGF, whereby the targeted agent(s) is internalized in a cell bearing the receptor.

- 17. The conjugate of any one of claims 1-16, for use as an active therapeutic substance.
- 18. The conjugate of any one of claims 1-16, for use in the manufacture of a medicament for treating a VEGF-mediated pathophysiological condition.
- 19. The conjugate of claim 18, wherein the pathophysiological condition is a dermatological disorder with underlying vascular proliferation, a solid tumor, or an ophthalmic disorder of the hyperproliferating blood vessels of the retina, iris, conjunctiva or vitreous humor.
- 20. The conjugate of any one of claims 1-16, for inhibiting proliferation of cells bearing VEGF receptors.
- 21. The conjugate of claim 12, for effecting gene therapy, wherein the conjugate includes a nuclear translocation sequence operatively linked to the targeted nucleic acid or VEGF.
- 22. A DNA fragment comprising a sequence of nucleotides encoding the conjugate of any one of claims 1-6 and 8-16.
  - 23. A plasmid, comprising the DNA of claim 22.
- 24. A plasmid of claim 23, wherein the plasmid is an expression vector for expression of the DNA encoding the conjugate in eukaryotic cells or is an expression vector for expression of the conjugate in prokaryotic cells.
  - 25. The plasmid of claim 24, wherein the vector is  $pP_1 \lambda$ .
- 26. A plasmid of claim 23, selected from the group consisting of PZ72B1. PZ73B1, PZ74B1, PZ74F5, PZ75B1, PZ75F5, PZ76B1, PZ76F5, PZ77B1, PZ78F5, PZ79B1, PZ79F5, PZ80B1, PZ81B1, PZ81B1, PZ82B1, PZ83B1, PZ84B1, PZ85B1, PZ85F5, PZ86B1, PZ95B1, PZ96B1, PZ97B1, PZ98B1, PZ99B1, PZ100B1, PZ101B1,

PZ102B1, PZ103B1, PZ104B1, PZ105B1, PZ106I1, PZ107I1, PZ108I1, PZ109J1, PZ110J1, PZ111J1, PZ112J1, PZ113J1 and PZ114J1.

- 27. A cell transfected or transformed with the expression vector of claim 24.
  - 28. The cell of claim 27 that is a bacterial cell.
- 29. A method of producing a conjugate of any one of claims 1-6 and 8-16. comprising culturing the cells of claim 27 under conditions whereby DNA is transcribed and translated to produce the conjugate.
- 30. A vascular endothelial cell growth factor monomer that is modified by insertion of a cysteine residue within about twenty amino acids of the N-terminus or C-terminus, wherein the inserted residue replaces a nonessential residue in the unmodified VEGF monomer or is added to the VEGF monomer.
- 31. The modified monomer of claim 30, wherein the cysteine residue is inserted within about 20 residues of the N-terminus.
- 32. The VEGF monomer of claim 46 that is VEGF CYS+4. VEGF CYS+2, or VEGF CYS-1.
  - 33. DNA encoding the VEGF monomer of claim 30.
- 34. A pharmaceutical composition, comprising the conjugate of any one of claims 1-16, in combination with a physiologically acceptable excipient.
  - 35. A method of producing a VEGF fusion protein comprising:
- (a) culturing cells transformed with a plasmid comprising pP<sub>L</sub>- $\lambda$  containing a DNA fragment according to claim 22, under conditions whereby the DNA fragment is transcribed and translated;
  - (b) lysing the cells to release inclusion bodies;
  - (c) solubilizing the inclusion bodies in a denaturant; and
  - (d) removing the denaturant, thereby refolding the fusion protein.
  - 36. A method of producing VEGF, comprising:

- (a) culturing cells transformed with a plasmid comprising  $pP_L$ - $\lambda$  containing a DNA fragment encoding VEGF, under conditions whereby the DNA fragment is transcribed and translated;
  - (b) lysing the cells to release inclusion bodies;
  - (c) solubilizing the inclusion bodies in a denaturant; and
  - (d) removing the denaturant, thereby refolding the fusion protein.

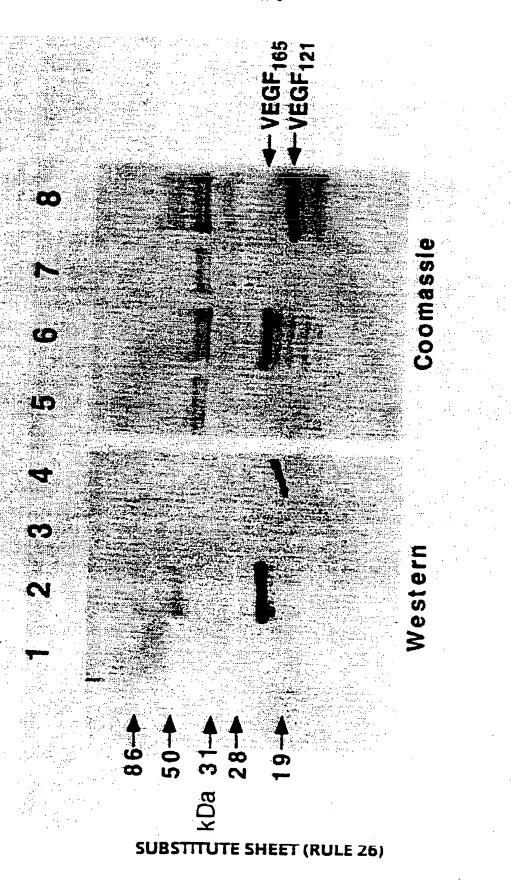
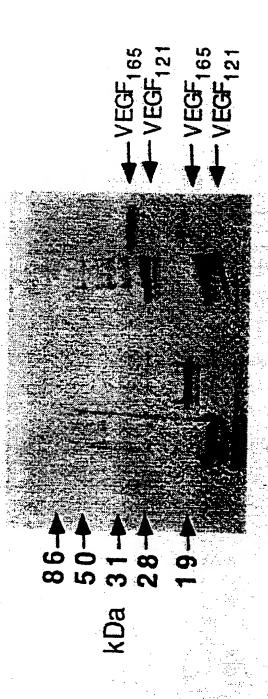


FIG. 1





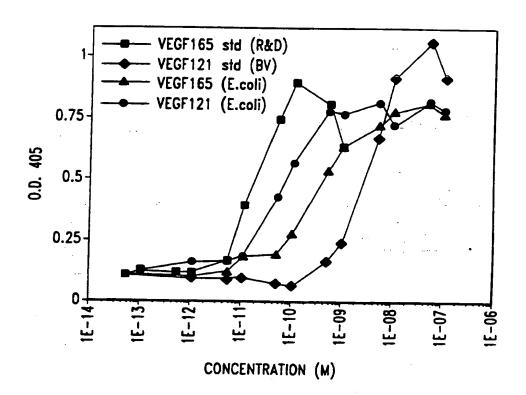
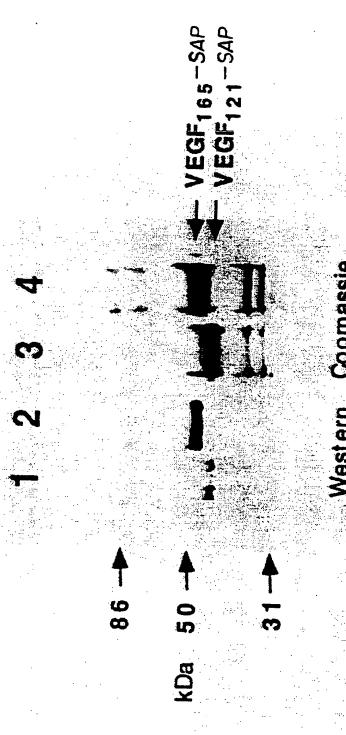
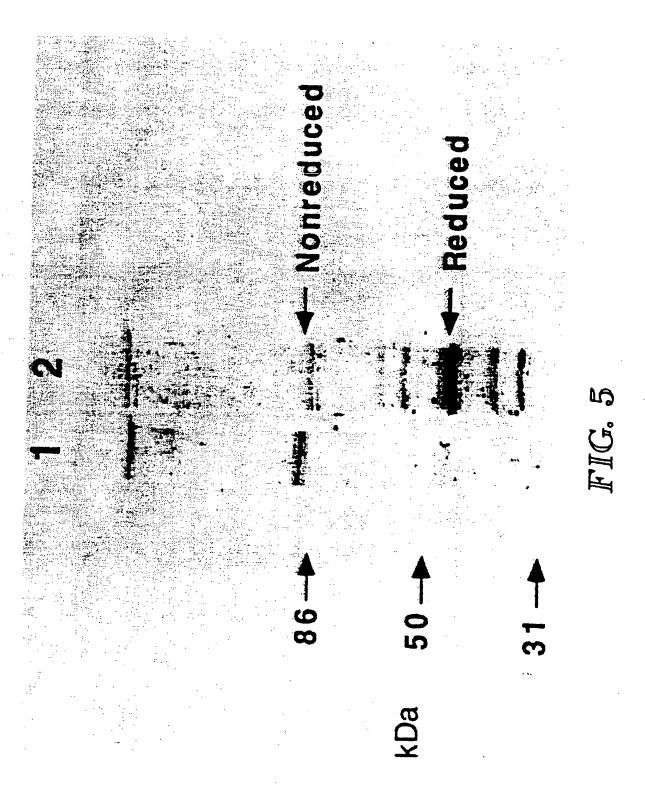


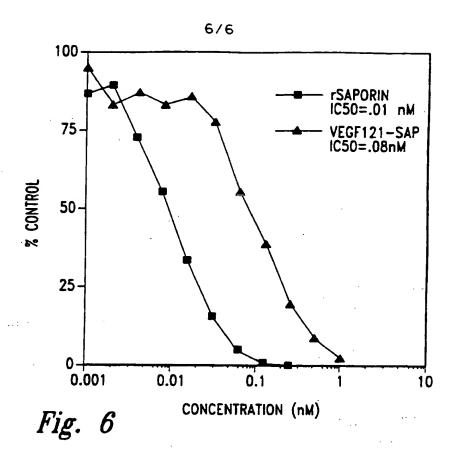
Fig. 3

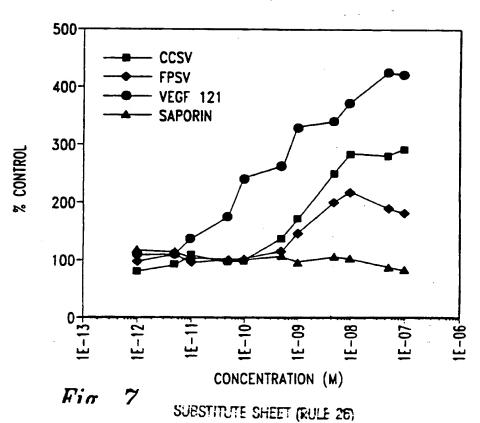






SUBSTITUTE SHEET (RULE 26)





## IONAL SEARCH REPORT

A. CLASSIFICATION OF SUBJECT MATTER IPC 6 A61K47/48 A61K41/00 C12N15/12 C12N1/21

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Name and mailing address of the ISA

C07K14/475

C07K19/00

C12N15/62

According to international Patent Classification (IPC) or to both national classification and IPC

#### B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols) IPC 6 A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

Category *	Catation of document, with indication, where appropriate, of	the relevant passages	Relevant to claim No.
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<b>K</b>	cited in the application see page 5, line 3 - line 30 see page 7, line 22 - line 27 see page 15, line 10 - line 13	; claims;	1-36
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X Furt	her documents are listed in the continuation of box C.	Patent family members are liste	ed in annex.
A docum connd E earlier filing L docum which custo O docum other P docum iater ti	ent which may throw doubts on priority claim(s) or is cited to establish the publication date of another in or other special reason (as specified) sent referring to an oral disclosure, use, exhibition or means ent published prior to the international filing date but han the priority date claimed	"T later document published after the sor priority date and not in conflict cited to understand the principle of invention."  "X" document of particular relevance; to cannot be considered novel or can movive an inventive step when the "Y" document of particular relevance; to cannot be considered to involve an document is combined with one or ments, such combination being obtain the art.  "&" document member of the same pair	with the application but theory underlying the he claimed invention not be considered to document is taken alone he claimed invention inventive step when the more other such document of the such document of a person skilled ent family
Date of the	actual completion of the international search	Date of mailing of the international	search report

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BERTE, M

# INTERNATIONAL SEARCH REPORT

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Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
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	FUNCTION OF VPF/VEGF.'	
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, P	JOURNAL OF BIOLOGICAL CHEMISTRY, vol.269, no.52, MD US pages 32879 - 32885 ANDY J. G. PÖTGENS, ET AL. 'COVALENT DIMERIZATION OF VASCULAR PERMEABILITY FACTOR /VASCULAR ENDOTHELIAL GROWTH FACTOR IS ESSENTIAL FOR ITS BIOLOGICAL ACTIVITY. EVIDENCE FROM CYS TOR SER MUTATIONS.'	Relevant to claim No.
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	see page 32879	
P,X	DATABASE BIOSIS BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US 95:186644 see abstract & 86TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, 18 March 1995, TORONTO, ONTARIO, CANADA & PROCEEDINGS OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH ANNUAL MEETING, vol.36, no.0, page 413 THIERRY A.R. ET AL. 'IN VITRO AND IN VIVO INHIBITION OF TUMORIGENICITY OF NEOPLASTIC	1-13, 17-20,34
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page 3 of 3



Int. ional application No.

PCT/US 95/ 10973

Box	1	Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)
This	inte	rnational search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:
1. [		Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:
2. [	X	Claims Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
		please see enclosed sheet!
3. [		Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).
Box	ı II	Observations where unity of invention is lacking (Continuation of item 2 of first sheet)
This	s Int	ernational Searching Authority found multiple inventions in this international application, as follows:
1		
1.		As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2.		As all searchable claims could be searches without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3.		As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
		COVERS ONLY MIDDE CARRIES FOR WHILE LEVEL HOLD PARTY P
		No required additional search fees were timely paid by the applicant. Consequently, this international search report is
4.		restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
Re	en af	k on Protest  The additional search fees were accompanied by the applicant's protest.
		No protest accompanied the payment of additional search fees.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

INCOMPLETE SEARCH OR MEANINGFUL SEARCH NOT POSSIBLE 2. Obscurities, Inconsistencies,...

In view of the large number of compounds which are defined by the general definition of claim 1,2,14 and dependent claims and also in view of the definition of products by means of their biological, chemical and/or pharmacological properties, the search had to be restricted for economic reasons.

The search was limited to the compounds for which pharmacological data was given and/or the compounds mentioned in the examples (see guidelines, Part B, Chapter III, paragraph 3.6)

Partially searched claims: 1-7,9,15,22,23,30,33,34

niormation on patent family members

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